

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:35:28 ; Search time 23.6027 Seconds
(without alignments)
1073.767 Million cell updates/sec

Title: US-09-831-907A-33
Perfect score: 641
Sequence: 1 MDKVPFCCLLFTGLNPLLS.....TRKHQHGGAPECFWKYCI 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	266.5	41.6	121	6 095J46	095J46 sus scrofa
2	239	37.3	139	4 08TA06	08TA06 homo sapien
3	175.5	27.4	85	6 095K72	095K72 sus scrofa
4	89	13.9	2249	5 09VCU9	09VCU9 drosophila
5	84.5	13.2	168	16 093J49	093J49 streptomyc
6	81.5	12.7	229	4 09HBP7	09HBP7 homo sapien
7	81.5	12.7	523	4 09BUV9	09BUV9 homo sapien
8	81	12.6	4899	5 09VR91	09VR91 drosophila
9	80.5	12.6	390	13 09PRE3	09PRE3 ambystoma m
10	80.5	12.6	404	13 09PRE5	09PRE5 ambystoma m
11	80.5	12.6	409	13 057582	057582 cynops pyrr
12	80.5	12.6	419	13 09PRE4	09PRE4 ambystoma m
13	80.5	12.6	423	13 057581	057581 cynops pyrr
14	80.5	12.6	433	13 09PRE6	09PRE6 ambystoma m
15	80.5	12.6	438	13 057584	057584 cynops pyrr
16	80.5	12.6	452	13 057583	057583 cynops pyrr

17	79	12.3	941	3 08TGA0	08TGA0 picchia past
18	76.5	11.9	367	4 096D73	096D73 homo sapien
19	76.5	11.9	391	4 09UFV4	09UFV4 homo sapien
20	76.5	11.9	394	4 08WYV1	08WYV1 homo sapien
21	75.5	11.8	111	17 0919V0	0919V0 aetopyrum p
22	75.5	11.8	317	10 022050	022050 actinidia d
23	75.5	11.8	663	16 08XJ3	08XJ3 escherichia
24	75.5	11.8	1054	11 08R5K3	08R5K3 mus musculu
25	75.5	11.8	1141	11 08R5K4	08R5K4 mus musculu
26	75	11.7	155	11 099M44	099M44 mus musculu
27	75	11.7	966	5 024170	024170 drosophila
28	75	11.7	966	5 024171	024171 drosophila
29	74.5	11.6	404	4 08WVZ8	08WVZ8 homo sapien
30	74	11.5	236	16 09KYU4	09KYU4 streptomyc
31	74	11.5	240	2 09F0V5	09F0V5 azotarcus sp
32	74	11.5	342	10 09X1Z6	09X1Z6 oryza sativ
33	73.5	11.5	233	13 P87389	P87389 triturus al
34	73.5	11.5	679	16 08X455	08X455 escherichia
35	73.5	11.5	680	11 08R370	08R370 mus musculu
36	73.5	11.5	6048	2 093H87	093H87 streptomyc
37	73.5	11.5	7463	16 0944X6	0944X6 streptomyc
38	73	11.4	201	5 09V422	09V422 drosophila
39	73	11.4	342	5 09U1L8	09U1L8 drosophila
40	73	11.4	346	5 09W5B0	09W5B0 drosophila
41	73	11.4	392	16 097M90	097M90 clostridium
42	73	11.4	429	4 09UR04	09UR04 homo sapien
43	73	11.4	596	4 09H1R3	09H1R3 homo sapien
44	73	11.4	632	11 062719	062719 ratus norv
45	73	11.4	761	4 09Y2L4	09Y2L4 homo sapien

ALIGNMENTS

RESULT 1

095J46 ID 095J46 PRELIMINARY; PRT; 121 AA.
AC 095J46;
DT 01-DEC-2001 (TREMUREL.19, Created)
DT 01-DEC-2001 (TREMUREL.19, Last sequence update)
DT 01-MAR-2002 (TREMUREL.20, Last annotation update)
DE Urotensin II transcript variant 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RX MEDLINE=20017983; PubMed=10548501;
RA Mori M., Sugo T., Abe M., Shimomura Y., Kurihara M., Kitada C.,
RA Kikuchi K., Shintani Y., Kurokawa T., Onda H., Nishimura O.,
RA Fujino M.;
RT "Urotensin II is the endogenous ligand of a G-protein-coupled orphan
receptor, SEUR (GPR14).";
RL Biochem. Biophys. Res. Commun. 265:123-129(1999).
DR EMBL; AB063245; BAB60888.1;
DR EMBL; AB063244; BAB60887.1;
DR InterPro; IPR001483; Urotensin-II.
DR Pfam; PF02083; Urotensin-II.
DR PROSITE; PS00984; UROTENSIN-II; UNKNOWN.1
SO SEQUENCE 121 AA; 13580 MW; 656EAB01AF6101B CMC64;

Query Match 41.6%; Score 266.5; DB 6; Length 121;
Best Local Similarity 49.1%; Pred. No. 1.8e-18;
Matches 57; Conservative 14; Mismatches 44; Indels 1; Gaps 1;

Oy 8 CLFTGLNPLLSPTVTGERTIQLPVLEDDALRALEELRMALLQTLRTMGTEAGES 67

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Db 7 CLLLCGLGLFALPVDSRKEPLPESA -PEDVRSAMDELERASLLQMLPETGAEAGD 65
QY 68 PCGAGSTETPTPRGSMRKAFACONSNTVLSRLARTRKOHKGHAPECFMKYCI 123
Db 66 LREADAGMDIFYPGRGEMRKAFSGODPNIFLSHLARIKPKYKRGPPSECFMKYCV 121

RESULT 2
Q8TAU6 PRELIMINARY: PRT: 139 AA.
AC Q8TAU6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
OS Similar to urolensin 2.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL, BC025776; AAH25776.1;
SQ SEQUENCE 139 AA; 16276 MW; 32DC529936D5BDB6 CRC64;

Query Match
Best Local Similarity 49.1%; Pred. No. 1e-15; Length 139;
Matches 55; Conservative 17; Mismatches 38; Indels 2; Gaps 1;

QY 1 MDKVPCCLLFTGLNPLSLPYDTGERTLQIPVEEDALRALPELERALLQTLQRTM 60
Db 1 MKVLASCCLLFTGLNPLSLPYDRETSFQSLAPHEARLPELERASLLQILPEML 60
QY 61 GTEAGSPEDACSTETTPPRGSMRK -APAGONSNTVLSRLARTRKOHQ 110
Db 61 GAERGDLRKADSTWTFNFRGNLRFQDFSGODPNILSLHLARIMKPKYK 112

RESULT 3
Q9SK72 PRELIMINARY: PRT: 85 AA.
AC Q9SK72;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Urolensin II transcript variant 2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN RN
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
(2)
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RX MEDLINE=20017983; PubMed=10548501;
RA Mori M., Sugo T., Abe M., Shimomura Y., Kurihara M., Kitada C.,
RA Kikuchi K., Shintani Y., Kurokawa T., Onda H., Nishimura O.,
RA Fujino M.;
RT "Urolensin II is the endogenous ligand of a G-protein-coupled orphan
RT receptor, SEUR (GPR14).";
RL Blochem. Biophys. Res. Commun. 265:123-129(1999).
DR EMBL, AB063246; BAB0889.1;
DR InterPro, IPR001483; Urolensin_II.
DR Pfam, PF02083; Urolensin_II; 1.
DR PROSITE, PS00984; UROLENSIN_II; UNKNOWN.1.
SQ SEQUENCE 85 AA; 9644 MW; F519CFEDFCBA863 CRC64;
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Query Match
Best Local Similarity 27.4%; Score 175.5; DB 6; Length 85;
Matches 40; Conservative 13; Mismatches 26; Indels 37; Gaps 2;

QY 8 CLFTGLNPLSLPYDTGERTLQIPVEEDALRALPELERALLQTLQRTMCTENGES 67
Db 7 CLLLCGLGLFALPVDSRKEPLP-----SDAG-- 36

QY 68 PCGAGSTETPTPRGSMRKAFACONSNTVLSRLARTRKOHKGHAPECFMKYCI 123
Db 37 -----MDIFYPGRGEMRKAFSGODPNIFLSHLARIKPKYKRGPPSECFMKYCV 85

RESULT 4
Q9VCU9 PRELIMINARY: PRT: 2249 AA.
AC Q9VCU9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG4792 protein.
GN DCR-1 OR CG4792.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyocera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zheng Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe C.R., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Bendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod W.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL, AE003740; AAF56056.1;
DR FlyBase, FBgn0039016; Dcr-1.
DR InterPro, IPR001410; DEAD.
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QY 42 RALEELERNAALLQTLQMTGEASPGESTPTPTPGSRKKAFAQONSMTVLSRL 101
 DB 105 RAQOEAEER-----ALQOARKGEQGGPPKASPSTAGETPSGVRLEPYDVLRLRLV 159
 QY 102 APTTKO-----HKQGAPECF 118
 DB 160 KPERQOQVPRKDYKSKVSLEF 180

RESULT 8
 Q9VR91 PRELIMINARY; PRT; 4899 AA.

AC Q9VR91
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE HERC2 protein.
 GN HERC2 OR CG11734.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthoptera; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RX MEDLINE=20196006; PubMed=10731132;
 RC STRAIN=BERKELEY;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostlin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalaal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Port V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spieler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaes R., Tecor C., Turner C., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA G1bbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003571; AAF50913.2;
 DR FLYBase: FB9n0031107; HERC2.
 DR InterPro: IPR000569; HECT_domain.
 DR InterPro: IPR000408; Reg_Chrt_condens.
 DR InterPro: IPR000449; UBA_domain.
 DR Pfam: PF00632; HECT; 1.
 DR Pfam: PF00415; RCC1; 15.

DR PRINTS; PR00633; RCNDNSATION.
 DR SMART; SM00119; HECTC; 1.
 DR PROSITE; PS50237; HECT; 1.
 DR PROSITE; PS00626; RCC1_2; UNKNOWN_4.
 DR PROSITE; PS0012; RCC1_3; 18.
 SQ SEQUENCE 4899 AA; 528653 MW; 2D10F54ABDF71FAC CRC64;

Query Match
 Best Local Similarity 28.5%; Score 81; DB 5; Length 4899;
 Matches 37; Conservative 14; Mismatches 43; Indels 36; Gaps 5;

QY 12 IGLIN-----PLSLPYDTGERTLOPLVEEDA-----LRAL----- 44
 DB 2072 LGWLNIGFTRAISGDCPRCLLESTRGWLSHTLSLEQFAGNAGYRQLHCLRLQLIL 2131

QY 45 -----ELEERM-ALLQTLQMTGEASPGESTPTPTPGSRKKAFAQONSMTVLS 98
 DB 2132 AQWGAEEPRMPALVHQLFATIGRIALHCPGDA---SLPTAGKARVLLTASHSGSVAE 2188

QY 99 RLARTRKQH 108
 DB 2189 ELVALRLRLH 2198

RESULT 9
 Q9PRE3 PRELIMINARY; PRT; 390 AA.

AC Q9PRE3
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAR-2001 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Paired-box transcription factor (Fragment).
 GN PAX6.
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RX [1]
 RA SEQUENCE FROM N.A.
 RA Glaser T.M., Walton D.S., Cai J., Epstein J.A., Jepeal L., Maas R.L.;
 RT "PAX6 gene mutations in aniridia.";
 RL (In) Wiggs J. (eds.);
 RL Molecular genetics of ocular disease, pp.52-82, Wiley Press,
 RL New York (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Glaser T.M.;
 RA Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
 CC - SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC - SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
 DR EMBL: AF159415; AAD50904.1; -.
 DR HSSP; P26367; 6PAX.
 DR InterPro: IPR001356; Homeobox.
 DR InterPro: IPR001523; Paired_box.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS; PR00292; PAX; 1.
 DR PRODOM; PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00351; PAX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS50071; HOMEBOX_2; 1.
 DR PROSITE; PS00034; PAIRED_BOX; 1.
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;
 KW Paired box; Transcription regulation.
 FT NON_TER 1
 SQ SEQUENCE 390 AA; 43548 MW; 37AF39F5CA3158B CRC64;

Query Match
 Best Local Similarity 12.6%; Score 80.5; DB 13; Length 390;
 Matches 26; Conservative 17; Mismatches 46; Indels 17; Gaps 2;

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OY 20 SLPTVDTGERTLOLVLEEDALRALELELMALLQTLRQTMGTAGESPGEGPSTETPT 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 114 NIPSVSSINRVLRLNLASEKQMGADGMVDKRLRLNGCOTGTGTRPGWPGTSVPG--OPT 171
OY 80 PRGSMKRAFAQONSNTV-----LSRLLATRKQHKQ 110
   | : : : : : : : : : : : : : : : : : : : : : : : :
DB 172 PDGCGQCGEGGENTNMISSNGEDSDAQMRLQKRLQRNRRTSFTQ 217

RESULT 10
O9PRE5 PRELIMINARY: PRT: 404 AA.
AC O9PRE5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Paired-box transcription factor +- isoform (Fragment).
GN PAX6.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Glaser T.M., Walton D.S., Cai J., Epstein J.A., Jepsal L., Maas R.L.;
RT "PAX6 gene mutations in aniridia.";
RL (in) Wiggs J. (eds.);
RL Molecular genetics of ocular disease, pp.52-82, Wiley Press,
RN New York (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Glaser T.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: AF169413; AAD50902.1; -
DR HSSP: P26367; 6PAX.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR Pfam: PF00292; PAX; 1.
DR PRINTS: PR00027; PAIREDBOX.
DR PRODOM: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00351; PAX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
KM DNA-binding; Homeobox; Nuclear protein.
FT NON-TER
SQ SEQUENCE 404 AA; 45073 MW; DE16D591EC314482 CRC64;

Query Match 12.6%; Score 80.5; DB 13; Length 404;
Best Local Similarity 24.5%; Pred. No. 9;
Matches 26; Conservative 17; Mismatches 46; Indels 17; Gaps 2;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RA Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;
RT "pax-6 gene expression in newt eye development.";
RL Dev. Genes Evol. 207:167-176(1997).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
DR EMBL: D88741; BAA24023.1; -
DR HSSP: P26367; 6PAX.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR Pfam: PF00292; PAX; 1.
DR PRINTS: PR00027; PAIREDBOX.
DR PRODOM: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00351; PAX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS50071; HOMEBOX_2; 1.
DR PROSITE: PS00034; PAIRED BOX; 1.
KM DNA-binding; Developmental protein; Homeobox; Nuclear protein;
KM Paired box; Transcription regulation.
SQ SEQUENCE 409 AA; 45855 MW; 5B1A5FD50F710510 CRC64;

Query Match 12.6%; Score 80.5; DB 13; Length 409;
Best Local Similarity 24.5%; Pred. No. 9.1;
Matches 26; Conservative 17; Mismatches 46; Indels 17; Gaps 2;

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OY 20 SLPTVDTGERTLOLVLEEDALRALELELMALLQTLRQTMGTAGESPGEGPSTETPT 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 NIPSVSSINRVLRLNLASEKQMGADGMVDKRLRLNGCOTGTGTRPGWPGTSVPG--QPT 190
OY 80 PRGSMKRAFAQONSNTV-----LSRLLATRKQHKQ 110
   | : : : : : : : : : : : : : : : : : : : : : : : :
DB 191 PDGCGQCGEGGENTNMISSNGEDSDAQMRLQKRLQRNRRTSFTQ 236

RESULT 12
O9PRE4 PRELIMINARY: PRT: 419 AA.
AC O9PRE4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Paired-box transcription factor (Fragment).
GN PAX6.
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Glaser T.M., Walton D.S., Cai J., Epstein J.A., Jepsal L., Maas R.L.;
RT "PAX6 gene mutations in aniridia.";
RL (in) Wiggs J. (eds.);
RL Molecular genetics of ocular disease, pp.52-82, Wiley Press,
RN New York (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Glaser T.M.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
DR EMBL: AF169414; AAD50903.1; -
DR HSSP: P26367; 6PAX.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR001523; Paired_box.
DR Pfam: PF00046; homeobox; 1.
DR Pfam: PF00292; PAX; 1.

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DR PRINTS; PR00027; PAIREDBOX.
 DR Prodom: PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00351; PAX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 DR PROSITE; PS00034; PAIRED_BOX; 1.
 DR DNA-binding; Developmental protein; Homeobox; Nuclear protein;
 KW Paired box; Transcription regulation.
 FT NON_TER
 SQ SEQUENCE 419 AA; 46161 MW; B35096F3AECB5F6D CRC64;

Query Match 12.6%; Score 80.5; DB 13; Length 419;
 Best Local Similarity 24.5%; Pred. No. 9.3;
 Matches 26; Conservative 17; Mismatches 46; Indels 17; Gaps 2;

QY 20 SLPTVDTGERTQLPVLLEEDALRLALELEERALLQTLROTMTGEAGSPGAGSTETPT 79
 DB 114 NIPSVSSINRYLRNLASEKQMGADGMYDKLRMLNGQTGTWGPVPGTSVPG--QPT 171
 QY 80 PGSMRKAFAAGNSNTV-----LSRLARTRKQHKQ 110
 DB 172 PDGCGQOEGGEGNTNMISSNGEDSDAQMRLQKRKLQRNRSTFTQ 217

RESULT 13
 ID 057581 PRELIMINARY; PRT; 423 AA.
 AC 057581;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE PAX6 LS.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;
 RT "pax-6 gene expression in newt eye development."
 RL Dev. Genes Evol. 207:167-176(1997).
 CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: D88741; BAA24022.1; -
 DR HSSP: P26367; 6PAX.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox.
 DR Pfam: PF00292; PAX; 1.
 DR PRINTS; PR00027; PAIREDBOX.
 DR Prodom: PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00351; PAX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 423 AA; 47363 MW; F4500FDE94BBB32 CRC64;

Query Match 12.6%; Score 80.5; DB 13; Length 423;
 Best Local Similarity 24.5%; Pred. No. 9.4;
 Matches 26; Conservative 17; Mismatches 46; Indels 17; Gaps 2;

QY 20 SLPTVDTGERTQLPVLLEEDALRLALELEERALLQTLROTMTGEAGSPGAGSTETPT 79
 DB 147 NIPSVSSINRYLRNLASEKQMGADGMYDKLRMLNGQTGTWGPVPGTSVPG--QPT 204
 QY 80 PGSMRKAFAAGNSNTV-----LSRLARTRKQHKQ 110
 DB 205 PDGCGQOEGGEGNTNMISSNGEDSDAQMRLQKRKLQRNRSTFTQ 250

RESULT 14
 Q9PRE6

ID Q9PRE6 PRELIMINARY; PRT; 433 AA.
 AC Q9PRE6;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Paired-box transcription factor ++ isoform (Fragment).
 GN PAX6.
 OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Glaser T.M., Walton D.S., Cai J., Epstein J.A., Jeepeal L., Maas R.L.;
 RT "PAX6 gene mutations in aniridia."
 RL (in) Wiggs J. (eds.);
 RL Molecular genetics of ocular disease, pp.52-82, Wiley Press,
 RL New York (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Glaser T.M.;
 RL submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 DR EMBL: AF169412; AAD50901.1; -
 DR HSSP: P26367; 6PAX.
 DR InterPro: IPR001356; Homeobox.
 DR Pfam: PF00046; homeobox; 1.
 DR PRINTS; PR00027; PAIREDBOX.
 DR Prodom: PD000010; Homeobox; 1.
 DR SMART; SM00389; HOX; 1.
 DR SMART; SM00351; PAX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.
 DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 FT NON_TER
 SQ SEQUENCE 433 AA; 47687 MW; B61ED5B1E733DB55 CRC64;

Query Match 12.6%; Score 80.5; DB 13; Length 433;
 Best Local Similarity 24.5%; Pred. No. 9.7;
 Matches 26; Conservative 17; Mismatches 46; Indels 17; Gaps 2;

QY 20 SLPTVDTGERTQLPVLLEEDALRLALELEERALLQTLROTMTGEAGSPGAGSTETPT 79
 DB 128 NIPSVSSINRYLRNLASEKQMGADGMYDKLRMLNGQTGTWGPVPGTSVPG--QPT 185
 QY 80 PGSMRKAFAAGNSNTV-----LSRLARTRKQHKQ 110
 DB 186 PDGCGQOEGGEGNTNMISSNGEDSDAQMRLQKRKLQRNRSTFTQ 231

RESULT 15
 ID 057584 PRELIMINARY; PRT; 438 AA.
 AC 057584;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE PAX6 LS.
 OS Cynops pyrrhogaster (Japanese common newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
 OX NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mizuno M., Takabatake T., Takahashi T.C., Takeshima K.;
 RT "pax-6 gene expression in newt eye development."
 RL Dev. Genes Evol. 207:167-176(1997).
 CC -I- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
 CC -I- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
 DR EMBL: D88741; BAA24025.1; -

DR HSSP: 26367; 6PAX.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR001523; Paired_box.
DR Pfam: PF00046; homeobox_1.
DR Pfam: PF00292; PAX; 1.
DR PRINTS: PR00027; PAIREDBOX.
DR ProDom: PD000010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR SMART: SM00351; PAX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS0071; HOMEBOX_2; 1.
DR PROSITE: PS00034; PAIRED_BOX; 1.
DR DNA-binding: Developmental protein; Homeobox; Nuclear protein;.
KW Paired box; Transcription regulation.
SQ SEQUENCE 438 AA; 4845 MW; B5146D49048B511 CRC64;

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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match

Best Local Similarity 44.28; Score 279.5; DB 9; Length 124;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY I MDRVPCCLIFVGLNDLSPYTDIGEMSLQPLVEENALRALEDELEPRLALQTLQTV 60
DB 1 MYLASCCLLETFGLNPLSLPLDLSREISFQLSAPHEADRLPELEFRASLIQILPEML 60
QY 61 GTEAGSLGADPSAETPPRGSLRK-ALTGDSNTVLSRLLAFTKRRKRGTAPECF 118
DB 61 GABRGILRKADSTINFRGNLRKFQDPSGDDPNILSLHLARLWKPYKRRKT-PDCF 119
QY 119 WKCV 123
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DB 120 WKYCV 124

RESULT 9

US-09-993-687-266

Sequence 266, Application US/09993687

Publication No. US20020198149A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2/30PIC11
CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04

RESULT 8
US-09-991-181-266
Sequence 266, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC53
CURRENT APPLICATION NUMBER: US/09/991,181
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2%; Score 279.5; DB 9; Length 124;
Best Local Similarity 49.6%; Pred. No. 1.4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;
QY I MDRVPCCLLVGLNPLISFPTDGEWSLQVLEENALRLERLETALQLTQRQV 60
DB I MKLASCCLEFTGLNPLISLPLDSREISFQLSAPHEARLTPPELERASLQIIPML 60
QY 61 GTEAEGSLGADPSAETPTPRGSLRK--ALTGDSMTVLSSRLAPRKOROHGAPECF 118
DB 61 GAERDILKRKADSSNIFNPRGNLKRKFQDESGDDPNILLSHLARIMWKPKKHEPDCF 119
QY 119 WKYCI 123
DB 120 WKYCV 124

PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
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PRIOR APPLICATION NUMBER: 60/090431
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2% Score 279.5; DB 9; Length 124;

Best Local Similarity 49.6%; Pred. No. 1.4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

OY 1 MDRVPECCLEFVGLNPLSPVDTGENSLOLVLEENALRALLEELEFTALLQTLROTV 60
DB 1 MYKLASCCLLFGFLNPLSLPLDLSREISFOLSAVHEDARLTPLELEVASLQILPEXL 60
OY 61 GTEAEGSLQADAPSAETPPRGSLSK--ALTGODSTTVLSRLLAIRKOROKHGTAPECF 118
DB 61 GAERDILKKAADSTNIENPRGNLRKRFODFSCODPNILLSHLARIWKPKKRET-PDCE 119
OY 119 WKYCI 123
DB 120 WKYCV 124

RESULT 7
US-09-990-436-266
Sequence 266, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Geider, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC14
CURRENT APPLICATION NUMBER: US/09/990,436
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

RESULT 6
US-09-989-730-266
Sequence 266, Application US/09989730
Publication No. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C69
CURRENT FILING DATE: 2001-11-20
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-10-17
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47	PRIOR FILING DATE:	1998-07-02
48	PRIOR APPLICATION NUMBER:	60/091633
49	PRIOR FILING DATE:	1998-07-02
50	PRIOR APPLICATION NUMBER:	60/091978
51	PRIOR FILING DATE:	1998-07-07
52	PRIOR APPLICATION NUMBER:	60/091982
53	PRIOR FILING DATE:	1998-07-07
54	PRIOR APPLICATION NUMBER:	60/092182
55	PRIOR FILING DATE:	1998-07-09

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Oy  61 GTEAESLCOADPSAETPTPRGSLAK - ALTGQDSNTVLSRLLTATRROROHGNAPECF 118
    | : : | | | | | | | : : : | : : |
Db  61 GAERGDILKKRADSSTIENFPRGNLKKFODFSQODPNILSLHLARIMKPYKKRET-PDCF 119
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Oy  119 WKYCI 123
    | | | | |
Db  120 WKYCV 124

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Sequence 266, Application US/0989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kjaevlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2/30PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2%; Score 279.5; DB 9; Length 124;
Best Local Similarity 49.6%; Pred. No. 1.4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

OY 1 MDPVFCCLLFVGLNPLSPVTDGEMSLQPVLENNALRLLEFLERLALQTLQRTQV 60
DB I MKYLASCCLLFVGLNPLSLPLDSREISFOLSAPEHDLRLPEELERASLQTLPEML 60
OY 61 GTEAEGSLQADPSAETPTPGSLRK--ALTGDSNTVLSRLATRRKORKHGTAPECF 118
DB 61 GAERGDLRKADSTNIFNDRGRLRKRFODESGDDPVLILSHLARIMKRYKKRET-PDCE 119
OY 119 WKYCI 123
DB 120 WKYCV 124

RESULT 4
US-09-989-735-266

PRIOR APPLICATION NUMBER: 60/090433	
PRIOR FILING DATE: 1998-06-24	
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PRIOR APPLICATION NUMBER: 60/091633	
PRIOR FILING DATE: 1998-07-02	
PRIOR APPLICATION NUMBER: 60/091978	
PRIOR FILING DATE: 1998-07-07	
PRIOR APPLICATION NUMBER: 60/091982	
PRIOR FILING DATE: 1998-07-07	
PRIOR APPLICATION NUMBER: 60/092182	
PRIOR FILING DATE: 1998-07-09	

Query Match	44.2%	Score 279.5;	DB 9;	Length 124:
Best Local Similarity	49.6%;	Pred. No. 1.4e-22;		
Matches	62;	Conservative	16;	Mismatches 44; Indels 3; Gaps 2
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Db	1	MYKLASCCLLFTGFNLNPLLSLPLDSDRETSFQLSNAPHEARLTPPELEFASLLQITPEML	60	
OY	61	GTEAEGSLGGADPSAEPTPPGSSLRK--ALTGODSNTVLSRLLAIRTKORKGHGAPECF	118	
		: : : : : ::::: ::::: : : : ::::: : : : :::::		
Db	61	GAERODILRRKADSSNTFNPNRGRLKKFDQESGDQDNILLSHLARIMKYKKRET-PDCF	119	
OY	119	WKYCI 123		
		: :::::		
Db	120	WKYCV 124		

RESULT 3
US-09-989-293A-266
Sequence 266, Application US/09989293A

Patent No US20020177164A1	GENERAL INFORMATION:
APPLICANT: Ashtkenazi, Avi J.	
APPLICANT: Baker, Kevin P.	
APPLICANT: Botstein, David	
APPLICANT: Desnoyers, Luc	
APPLICANT: Eaton, Dan L.	
APPLICANT: Ferrara, Napoleone	
APPLICANT: Fong, Sherman	
APPLICANT: Gerber, Hanspeter	
APPLICANT: Gerlitsen, Mary E.	
APPLICANT: Goddard, Audrey	
APPLICANT: Godowski, Paul J.	
APPLICANT: Grimaldi, J. Christopher	
APPLICANT: Gurney, Austin L.	
APPLICANT: Kljavin, Ivar J.	
APPLICANT: Napier, Mary A.	
APPLICANT: Pan, James	
APPLICANT: Paoni, Nicholas F.	
APPLICANT: Roy, Margaret Ann	
APPLICANT: Stewart, Timothy A.	
APPLICANT: Tumas, Daniel	
APPLICANT: Watanabe, Colin K.	
APPLICANT: Williams, P. Mickey	
APPLICANT: Wood, William I.	
APPLICANT: Zhang, Zemin	
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
TITLE OF INVENTION: Acids Encoding the Same	
FILE REFERENCE: P2730PIC66	
CURRENT APPLICATION NUMBER: US/09/989,293A	
CURRENT FILING DATE: 2001-11-20	
PRIOR APPLICATION NUMBER: 60/049787	
PRIOR FILING DATE: 1997-06-16	
PRIOR APPLICATION NUMBER: 60/062250	
PRIOR FILING DATE: 1997-10-17	
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PRIOR APPLICATION NUMBER: 60/088030	
PRIOR FILING DATE: 1998-06-04	
PRIOR APPLICATION NUMBER: 60/088033	
PRIOR FILING DATE: 1998-06-04	

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
PRIOR FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24

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APPLICATION NUMBER: US 899,241
FILING DATE: 22-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 746,121
FILING DATE: 15-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US90/07641
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 585,471
FILING DATE: 20-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 455,611
FILING DATE: 22-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 609,157
FILING DATE: 02-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 557,517
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Luann Csegr
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2972
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 893 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-977-434-4

Query March 11.3%; Score 71.5; DB 1; Length 893;
Best Local Similarity 28.6%; Pred. NO. 9;
Matches 28; Conservative 15; Mismatches 28; Indels 27; Gaps 5.

QY 24 TDTGEMSLQPVLEENA-----LRALEELERT--ALLQTLROTVGT----- 62
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QY 63 --EAGSGAQADPSAE---TTPPRKG-SLRKALTGQDSN 94
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Db 629 TGTATGTRLSSDPNLQNLPKSEEGEKRIKAIIVDPDN 666
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Search completed: March 10, 2003, 17:48:12
Job time : 12.3027 secs

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,160
FILING DATE: 06-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (To be assigned)
FILING DATE: 06-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0942.4250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 893 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-019-160-7

Query Match 11.5%; Score 72.5; DB 4; Length 893;
Best Local Similarity 28.9%; Pred. No. 6.8;
Matches 28; Conservative 15; Mismatches 25; Indels 29; Gaps 5;

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Db 569 TKTEGYSTRIVLEINAEHIEIVPLILEYRKIQKIKST-YIDTLPLKLVNPTGTGRIHASFH 627
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QY 64 ----AEGSLGQADPSAE---TPPRG-SLRKALTGOD 92
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RESULT 13
US-09-019-160-8
Sequence 8, Application US/09019160
Patent No. 6306588
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
APPLICANT: Solus, Joseph
APPLICANT: Yang, Shuwei
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,160
FILING DATE: 06-FEB-1998

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (To be assigned)
FILING DATE: 06-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.4250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 893 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-019-160-8

Query Match 11.5%; Score 72.5; DB 4; Length 893;
Best Local Similarity 28.9%; Pred. No. 6.8;
Matches 28; Conservative 15; Mismatches 25; Indels 29; Gaps 5;

QY 24 TDGEMSLQPLVEENA-----LRALELEPRTALLQTLRQVTGTE----- 63
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Db 569 TKTEGYSTRIVLEINAEHIEIVPLILEYRKIQKIKST-YIDTLPLKLVNPTGTGRIHASFH 627
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QY 64 ----AEGSLGQADPSAE---TPPRG-SLRKALTGOD 92
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 628 QTGTATGRLSSDPNLQNLPTKSEGEIKRAIYPOD 664
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RESULT 14
US-09-019-160-9
Sequence 9, Application US/09019160
Patent No. 6306588
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
APPLICANT: Solus, Joseph
APPLICANT: Yang, Shuwei
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,160
FILING DATE: 06-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (To be assigned)
FILING DATE: 06-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,393
FILING DATE: 07-FEB-1997
CLASSIFICATION:


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RESULT 5
US-09-006-535-4
Sequence 4, Application US/09006535
Patent No. 5965396
GENERAL INFORMATION:
APPLICANT: Julie Yan Pan
APPLICANT: Mark Egerton
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN LYMPH NODE DERIVED GTPase
FILE REFERENCE: PHM 70295
CURRENT APPLICATION NUMBER: US/09/006.535
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows, Version 3.0
SEQ ID NO 4
LENGTH: 297
TYPE: PRT
ORGANISM: Mus musculus
US-09-006-535-4

Query Match 11.6%; Score 73.5; DB 2; Length 297;
Best Local Similarly 31.9%; Pred. No. 1.1;
Matches 22; Conservative 12; Mismatches 26; Indels 9; Gaps 2;

OY 55 TLRQTVGTEAGSLGQA-----DPSAETPPRGSILRKALTGODSNVYLRLARTKROR 108
Db 226 TLQHNVELEFGVVRQLRLRHODNAPETPSR---RRASLGQRARRRLALTRASARR 282
OY 109 KOHGTAPEC 117
Db 283 ALKARSKC 291

RESULT 6
US-09-019-160-4
Sequence 4, Application US/09019160
Patent No. 6306588
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
APPLICANT: Solus, Joseph
APPLICANT: Yang, Shuwel
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
TITLE OF INVENTION: Nucleic Acid Fragments and Uses Thereof
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019.160
FILING DATE: 06-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (To be assigned)
FILING DATE: 06-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037.393
FILING DATE: 07-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.4250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-019-160-4

Query Match 11.5%; Score 72.5; DB 4; Length 610;
Best Local Similarly 28.9%; Pred. No. 4;
Matches 28; Conservative 15; Mismatches 25; Indels 29; Gaps 5;

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Db 286 TKTGEYSTRILEVINHEIVPLILEYRKIQKLSF-YIDTLPLKLVNPKTGRIHASFH 344
OY 64 ---AEGSLGADPSAE---TPTPRG-SLRKALIGOD 92
Db 345 QTGTATGRLSSDPNLQNLPTKSEGEKIRKAIYPOD 381

RESULT 7
US-09-019-160-10
Sequence 10, Application US/09019160
Patent No. 6306588
GENERAL INFORMATION:
APPLICANT: Chatterjee, Deb K.
APPLICANT: Solus, Joseph
APPLICANT: Yang, Shuwel
TITLE OF INVENTION: Polymerases for Analyzing or Typing Polymorphic
TITLE OF INVENTION: Nucleic Acid Fragments and Uses Thereof
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019.160
FILING DATE: 06-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (To be assigned)
FILING DATE: 06-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037.393
FILING DATE: 07-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0942.4250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 610 amino acids

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:37:08 ; Search time 11.3027 Seconds
(Without alignments)
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Title: US-09-831-907A-30
Perfect score: 633
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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	198.5	31.4	139	US-09-477-071-2	Sequence 2, Appl1
3	187.5	29.6	103	US-09-027-381-4	Sequence 4, Appl1
4	187.5	29.6	103	US-09-477-071-4	Sequence 4, Appl1
5	73.5	11.6	297	US-09-006-535-4	Sequence 4, Appl1
6	72.5	11.5	610	US-09-019-160-4	Sequence 4, Appl1
7	72.5	11.5	610	US-09-019-160-10	Sequence 10, Appl1
8	72.5	11.5	677	US-09-019-160-3	Sequence 3, Appl1
9	72.5	11.5	708	US-09-019-160-5	Sequence 5, Appl1
10	72.5	11.5	893	US-09-019-160-2	Sequence 2, Appl1
11	72.5	11.5	893	US-09-019-160-6	Sequence 6, Appl1
12	72.5	11.5	893	US-09-019-160-7	Sequence 7, Appl1
13	72.5	11.5	893	US-09-019-160-8	Sequence 8, Appl1
14	72.5	11.5	893	US-09-019-160-9	Sequence 9, Appl1
15	71.5	11.3	893	US-07-977-434-4	Sequence 4, Appl1
16	71.5	11.3	893	US-08-458-819-4	Sequence 4, Appl1
17	71.5	11.3	893	US-09-105-697-10	Sequence 10, Appl1
18	71.5	11.3	893	PCR-US91-07035-4	Sequence 4, Appl1
19	69	10.9	740	US-08-971-089-6	Sequence 6, Appl1
20	69	10.9	740	US-09-022-983-5	Sequence 5, Appl1
21	68	10.9	2289	US-09-051-019-2	Sequence 2, Appl1
22	68	10.7	542	US-08-935-855-22	Sequence 22, Appl1
23	67.5	10.7	319	US-08-149-975A-2	Sequence 2, Appl1
24	66.5	10.5	494	US-08-484-661A-39	Sequence 39, Appl1
25	66.5	10.5	494	US-08-656-664-39	Sequence 39, Appl1
26	66.5	10.5	494	PCR-US96-09641-39	Sequence 39, Appl1
27	66.5	10.5	571	US-08-484-661A-37	Sequence 37, Appl1

ALIGNMENTS

28	66.5	10.5	571	3	US-08-656-664-37	Sequence 37, Appl1
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34	66.5	10.5	610	3	US-08-484-661A-16	Sequence 16, Appl1
35	66.5	10.5	610	3	US-08-484-661A-19	Sequence 19, Appl1
36	66.5	10.5	610	3	US-08-484-661A-23	Sequence 23, Appl1
37	66.5	10.5	610	3	US-08-484-661A-26	Sequence 26, Appl1
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44	66.5	10.5	610	3	US-08-656-664-23	Sequence 23, Appl1
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RESULT 1
US-09-027-381-2
; Sequence 2, Application US/09027381
; Patent No. 6075137
; GENERAL INFORMATION:
; APPLICANT: CULP, JEFFREY
; APPLICANT: MCNUITY, DEAN
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN UROTENSIN II
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,381
; FILING DATE: 20-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/072,383
; FILING DATE: 09-JAN-1998
; APPLICATION NUMBER: GP-70366-1P
; FILING DATE: 04-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET INFORMATION:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ. ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-027-381-2
Query Match 31.4%; Score 198.5; DB 3; Length 139;
Best Local Similarity 48.0%; Pred. No. 5e-16;

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DB 1 MYKLASCCLEFTGFLNPLSLPLDREISFQLSAPHEDARLTPELEFRASLIQILPEML 60
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DT 02-APR-2001 (first entry)
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DE Human PRO1068 (UNQ525) protein sequence SEQ ID NO:266.
XX
KW Human; secreted and transmembrane protein; PRO; cytosolic;
KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN WO200073454-A1.
XX
PD 07-DEC-2000.
XX
PE 30-MAR-2000; 2000WO-US08439.
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PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21090.
PR 08-OCT-1999; 99WO-US21547.
PR 30-NOV-1999; 99US-0158663.
PR 01-DEC-1999; 99WO-US28313.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US03565.
PR 22-FEB-2000; 2000WO-US04341.
PR 24-FEB-2000; 2000WO-US04914.
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PR 02-MAR-2000; 2000WO-US05004.
PR 15-MAR-2000; 2000WO-US05841.
PR 20-MAR-2000; 2000WO-US06884.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gertlisen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin LJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
WPI: 2001-032160/04.
DR N-PSDB: AAF44193.
XX
PT PRO polynucleotides used to produce polypeptides used to target

```

```

PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 12; Fig 184; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.
XX
SQ Sequence 124 AA:

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Query Match 44.2%; Score 279.5; DB 22; Length 124;
Best Local Similarity 49.6%; Pred. No. 6e-23;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

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DB 1 MYKLASCCLEFTGFLNPLSLPLDREISFQLSAPHEDARLTPELEFRASLIQILPEML 60
QY 61 GTEAEGSLGADPSAETPTPGSLRK--ALTGDSNTVLSRLARTRKORHGTAPCECF 118
DB 61 GAERGDILRKADSTNIFNPRGNLRKRFQDSGQDPNILLSHLARIMPKRKRET-PDCE 119
QY 119 WKYCI 123
DB 120 WKYCV 124

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Job time : 29.9189 secs

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KM pharmaceutical: receptor immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX MO9963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99MO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
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PR 22-JUN-1998; 98US-0090246.
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PR 01-JUL-1998; 98US-0091358.
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PR 07-JUL-1998; 98US-0091673.
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PR 09-JUL-1998; 98US-0091982.
PR 10-JUL-1998; 98US-0092182.
PR 20-JUL-1998; 98US-00932472.
PR 30-JUL-1998; 98US-0093339.
PR 04-AUG-1998; 98US-0094651.
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PR 12-AUG-1998; 98US-0096329.
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PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
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PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 31-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.

PR	26-NOV-1998:	98FR-0014914.	
XX			
PA	(INRM) INST NAT SANTE & RECH MEDICALE.		
XX			
PI	Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;		
XX			
DR	WPI: 2000-400075/34.		
XX	N-PSDB: AAAA6698.		
PT	New mammalian urotensin II polypeptide, useful for treating		
PS	neurodegeneration and spinal cord injury -		
XX	Claim 2; Fig 2; 42pp; French.		
CC			
CC	The present sequence represents a human prepro-urotensin II polypeptide.		
CC	in mammals, urotensin II promotes survival and regeneration of motor		
CC	neurons, and also has a hypertensive effect. The urotensin II		
CC	polypeptides and polynucleotides are useful for treating		
CC	neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,		
CC	para-plegia or amyotrophic lateral sclerosis). The polypeptides		
CC	are also used to screen for specific inhibitors, i.e. potential		
CC	antihypertensive agents.		
SO	Sequence 124 AA;		
Query Match	44.6%; Score 282.5; DB 21; Length 124;		
Best Local Similarity	49.6%; Pred. No. 2,8e-23;		
Matches 62; Conservative 17; Mismatches 43; Indels 3; Gaps			
OY	1 MDRVPFCLLVGLINPLSPVYDGTGMSQLPVLLENMLRALEELRVALLOTLPQTV 60		
DB	1 MYKLASCLLTGFLNPLSLPLDSRISFQISAPHEDKRLPEELERASLLQIPEML 60		
OY	61 GTEAGSLGQADPAETPTPGSLRK--ALTGQDSNTVLSRLARTKORKKHGTABECF 118		
DB	61 GAERQDILRKADSSNINPRGNLRKRGDDFGQDPNILLSHLARIKPKKKRET-PDCF 119		
OY	119 WKYCI 123		
DB	120 WKYCV 124		
RESULT 12			
AY87319			
ID	AAV87319 standard; protein; 124 AA.		
AC			
XX	AAV87319;		
XX			
DT	11-MAY-2000 (first entry)		
XX			
DE	Human signal peptide containing protein HSP-96 SEQ ID NO:96.		
XX			
KW	Human; signal peptide-containing protein; HSP; diagnosis; cancer;		
KW	Inflammation; cardiovascular disease; anticancer; anti-inflammatory;		
KW	antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;		
KW	antithrombotic; gene therapy; cell proliferation; neurological disorder;		
KW	reproductive disorder; developmental disorder; arteriosclerosis;		
KW	clrhrosis; psoriasis; acquired immune deficiency syndrome; anemia;		
KW	asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;		
KW	Parkinson's disease; Huntington's disease; ovulatory defect;		
XX	muscular dystrophy.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200000610-A2.		
XX			
PD	06-JAN-2000.		
XX			
PE	25-JUN-1999; 99WO-US14484.		
XX			
XX	26-JUN-1998; 98US-0090762.		
PR	31-JUL-1998; 98US-0094983.		

Query Match	44.6%	Score 282.5	DB 21	Length 124
Best Local Similarity	49.6%	Pred. No. 2.8e-23		
Matches	62	Conservative	17	Mismatches 43; Indels 3; Gaps 2;
Qy	1	MDRVPPCLLVYGLNPLSPVDTGSEMSLQVLYEENALRALEDELRATLLQRLQTV	60	
Db	1	MYKLASCCLLFGFNPPLSLPLRLSDRSREISFQLSAPHEBARLTPEELERASVLLQILPEWL	60	
Qy	61	GFVEAGSLGQADPSPATETPPRGSLSAK--ALTGQDSNTVLSRLLATRRQRKHGAPAEF	118	
Db	61	GAERGDILRAKADSNTINFPNGRLKRFQDFSGQADNIIILSHLAEIKWPKYKRET--PDCF	119	
Qy	119	WKYCI 123		
Db	120	WKYCV 124		

RESULT 13
AAV66707
ID AAV66707 standard: protein: 124 AA.
XX AAV66707:
XX
XX 05-APR-2000 (first entry)
XX
DE Membrane-bound protein PRO1068.
XX
KW Membrane-bound polypeptide: PRO polypeptide: LDU receptor: TIE ligand:

DR WPI: 2000-412287/35.
 XX
 PT Urotensin peptides which are ligands for sensory epithelium
 PT neuropeptide-like receptor (SENR) for diagnosis and treatment of
 PT hypertension
 XX
 PS Example 36: Page 140-141; 147pp; Japanese.
 XX
 CC The present invention provides peptides which are ligands for sensory
 CC epithelium neuropeptide-like receptor (SENR), and their amides, esters
 CC and salts. SENR is a G-protein coupled receptor protein (also known as
 CC GPR14), and the peptides which are ligands for it are forms of the
 CC peptide hormone urotensin II. The peptides can be used in the treatment
 CC and diagnosis of hypertension and kidney disease, and the development of
 CC drugs which are regulators of central functions, circulatory functions,
 CC heart functions, immune system functions, digestive functions, metabolic
 CC functions and genital functions. The present sequence represents a
 CC bovine SENR ligand protein from the present invention.
 XX
 SQ Sequence 122 AA;
 Query Match 46.4%; Score 293.5; DB 21; Length 122;
 Best Local Similarity 49.6%; Pred. No. 1.7e-24;
 Matches 61; Conservative 17; Mismatches 44; Indels 1; Gaps 1;
 QY 1 MDRVPCCLLVGLINPLSPFVDTGEMSLQVLEENALRALEELERTALLQTLRQTV 60
 Db 1 MYKLVSCLLFGLSINPLSLPVLDLSROESLQ-LAPEDVRSSTLDLERRASLLQMLPEMS 59
 QY 61 GTEAGSGQADPSAETPTPGSLRKALTGODSNVLSRLARTRKORHGTAECEFWK 120
 Db 60 GAETGEGLRNTDPTINIFYPRGNMRKAFSGDPKFLSDLSLRKQSKRGPSSSECEFWK 119
 QY 121 YCI 123
 Db 120 YCV 122
 RESULT 10
 AAU80120
 ID AAU80120 standard; Protein; 122 AA.
 AC AAU80120;
 XX
 DT 07-OCT-2002 (first entry)
 DE Cow sensory epithelium neuropeptide-like receptor (SENR) protein.
 XX
 KW SENR: Sensory epithelium neuropeptide-like receptor; cow; fear;
 KW attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
 KW schizophrenia; G protein-coupled; receptor.
 XX
 OS Bos taurus.
 XX
 PN WO200214513-A1.
 PD 21-FEB-2002.
 PF 10-AUG-2001; 2001WO-JP06899.
 XX
 PR 10-AUG-2000; 2000JP-0247968.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Matsumoto Y, Watanabe T, Takahashi H, Mori M;
 XX
 DR WPI: 2002-329576/36.
 XX
 PT Polypeptide GPR12 with ligand activity to sensor epithelium
 PT neuropeptide-like receptor, useful e.g. in treating attention deficit
 PT disorder or narcolepsy, or for screening drug candidates for these
 PT indications and for anxiety

PS Claim 6: Page 276; 290pp; Japanese.
 XX
 CC This invention relates to an anti-attention deficit disorder or anti-
 CC narcolepsy agent containing a polypeptide with a sequence identical or
 CC substantially similar to a fully defined 12 amino acid sequence given in
 CC the specification, and its amide, ester or their salt. The peptides
 CC have ligand activity to sensory epithelium neuropeptide-like receptor
 CC (SENR) protein. The invention also includes a method for diagnosing
 CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
 CC schizophrenia or fear. The polypeptides of the invention, their
 CC precursor proteins and their encoding DNAs are useful in treating
 CC attention deficit disorder or narcolepsy, or for screening drug
 CC candidates for these indications and for anxiety, depression, insomnia,
 CC schizophrenia or fear. They are also useful for gene therapy. The
 CC polypeptide is a G protein-coupled receptor protein, with ligand
 CC activity to sensor epithelium neuropeptide-like receptor. The present
 CC sequence represents the cow sensory endothelium neuropeptide-like
 CC receptor protein of the invention.
 XX
 SQ Sequence 122 AA;
 Query Match 46.4%; Score 293.5; DB 23; Length 122;
 Best Local Similarity 49.6%; Pred. No. 1.7e-24;
 Matches 61; Conservative 17; Mismatches 44; Indels 1; Gaps 1;
 QY 1 MDRVPCCLLVGLINPLSPFVDTGEMSLQVLEENALRALEELERTALLQTLRQTV 60
 Db 1 MYKLVSCLLFGLSINPLSLPVLDLSROESLQ-LAPEDVRSSTLDLERRASLLQMLPEMS 59
 QY 61 GTEAGSGQADPSAETPTPGSLRKALTGODSNVLSRLARTRKORHGTAECEFWK 120
 Db 60 GAETGEGLRNTDPTINIFYPRGNMRKAFSGDPKFLSDLSLRKQSKRGPSSSECEFWK 119
 QY 121 YCI 123
 Db 120 YCV 122
 RESULT 11
 AA93639
 ID AA93639 standard; Protein; 124 AA.
 XX
 AC AA93639;
 XX
 DT 25-SEP-2000 (first entry)
 DE Amino acid sequence of a human prepro-urotensin II (UII) polypeptide.
 XX
 KW Urotensin II; motor neuron; hypertensive; neurodegeneration;
 KW spinal cord trauma; hemi-plegia; para-plegia;
 KW amyotrophic lateral sclerosis; antihypertensive agent.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "signal peptide"
 FT Peptide 21..110
 FT /note= "pro-segment of urotensin II"
 FT Misc-difference 46 /note= "encoded by GAC"
 FT Misc-difference 47 /note= "encoded by GTA"
 FT Misc-difference 81 /note= "encoded by ATT"
 FT Peptide 114..124 /note= "urotensin II"
 XX
 PN WO200031265-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 26-NOV-1999; 99WO-FR02941.

```

FT      Peptide      /note= "pro-segment"
FT      90..103
FT      /note= "urotensin II peptide"
XX      WO200031265-A1.
XX      02-JUN-2000.
XX      26-NOV-1999; 99WO-FR02941.
XX      26-NOV-1998; 98FR-0014914.
XX      (INRM ) INST NAT SANTE & RECH MEDICALE.
XX      Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;
XX      WPI: 2000-400075/34.
XX      N-PSDB; AAA46711.
XX      New mammalian urotensin II polypeptide, useful for treating
XX      neurodegeneration and spinal cord injury -
XX      Claim 2; Page 30-31; 42pp; French.
XX      The present sequence represents a rat pro-urotensin II polypeptide.
XX      In mammals, urotensin II promotes survival and regeneration of motor
XX      neurons, and also has a hypertensive effect. The urotensin II
XX      polypeptides and polynucleotides are useful for treating
XX      neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
XX      para-plegia or amyotrophic lateral sclerosis). The polypeptides
XX      are also used to screen for specific inhibitors, i.e. potential
XX      antihypertensive agents.
XX      Sequence 103 AA:
XX      Query Match      82.9%; Score 525; DB 21; Length 103;
XX      Best Local Similarity 100.0%; Pred. NO. 3.8e-50;
XX      Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      21 FPYVDIGEMSLQPVLEENALRALEELERLALLQTLRQTGTAEAGSLGQADPSAETPTP 80
XX      1 FPYVDIGEMSLQPVLEENALRALEELERLALLQTLRQTGTAEAGSLGQADPSAETPTP 60
XX      DB      81 RGSRLKALTGQDSNTVLSRLARTRKORKHGTAPCECFMKYCI 123
XX      61 RGSRLKALTGQDSNTVLSRLARTRKORKHGTAPCECFMKYCI 103
XX      RESULT 8
XX      AAY93648
XX      ID AAY93648 standard; Protein; 103 AA.
XX      AC AAY93648;
XX      XX
XX      25-SEP-2000 (first entry)
XX      DE Amino acid sequence of murine pro-urotensin II (UII) polypeptide.
XX      KW Urotensin II; motor neuron; hypertensive; neurodegeneration;
XX      KW spinal cord trauma; hemi-plegia; para-plegia;
XX      KW amyotrophic lateral sclerosis; antihypertensive agent.
XX      OS Mus sp.
XX      XX
XX      Key      Location/Qualifiers
XX      FT      Peptide      1..86
XX      FT      /note= "pro-segment"
XX      FT      Peptide      87..103
XX      FT      /note= "urotensin II"
XX      MO200031265-A1.
XX      PD      02-JUN-2000.

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XX      26-NOV-1999; 99WO-FR02941.
XX      26-NOV-1998; 98FR-0014914.
XX      (INRM ) INST NAT SANTE & RECH MEDICALE.
XX      Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;
XX      WPI: 2000-400075/34.
XX      N-PSDB; AAA46720.
XX      New mammalian urotensin II polypeptide, useful for treating
XX      neurodegeneration and spinal cord injury -
XX      Claim 2; Page 32; 42pp; French.
XX      The present sequence represents a murine pro-urotensin II polypeptide.
XX      In mammals, urotensin II promotes survival and regeneration of motor
XX      neurons, and also has a hypertensive effect. The urotensin II
XX      polypeptides and polynucleotides are useful for treating
XX      neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
XX      para-plegia or amyotrophic lateral sclerosis). The polypeptides
XX      are also used to screen for specific inhibitors, i.e. potential
XX      antihypertensive agents.
XX      Sequence 103 AA:
XX      Query Match      68.6%; Score 434; DB 21; Length 103;
XX      Best Local Similarity 83.3%; Pred. NO. 4.2e-40;
XX      Matches 85; Conservative 6; Mismatches 11; Indels 0; Gaps 0;
XX      QY      22 PVTDTGEMSLQPVLEENALRALEELERLALLQTLRQTGTAEAGSLGQADPSAETPTP 81
XX      2 PVTDTGEMSLQPVLEENALRALEELERLALLQTLRQTGTAEAGSLGQADPSAETPTP 61
XX      DB      82 GSLRKALTGQDSNTVLSRLARTRKORKHGTAPCECFMKYCI 123
XX      62 GSKRAFAFGQNSNTVLSRLARTRKORKHGTAPCECFMKYCI 103
XX      RESULT 9
XX      AAB12501
XX      ID AAB12501 standard; Protein; 122 AA.
XX      AC AAB12501;
XX      XX
XX      27-OCT-2000 (first entry)
XX      DE Bovine SENR ligand protein sequence SEQ ID NO:29.
XX      KW SENR; sensory epithelium neuropeptide-like receptor; urotensin II;
XX      KW diagnosis; G protein-coupled receptor; hypertension; GPR14; hormone;
XX      KW kidney disease; regulator; central function; circulatory function;
XX      KW heart function; immune system function; digestive function;
XX      KW metabolic function; genital function.
XX      OS Bos taurus.
XX      XX
XX      WO200032627-A1.
XX      PD      08-JUN-2000.
XX      29-NOV-1999; 99WO-JP06649.
XX      30-NOV-1998; 98JP-0338984.
XX      PR      04-FEB-1999; 99JP-0026848.
XX      PR      26-AUG-1999; 99JP-0239367.
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX      Mori M, Abe M, Shimomura Y, Sugo T, Kitada C;

```

[illegible]

DR WPI: 2002-329576/36.

XX polypeptide GPR12 with ligand activity to sensor epithelium
XX neuropeptide-like receptor, useful e.g. in treating attention deficit
PT disorder or narcolepsy, or for screening drug candidates for these
PT indications and for anxiety

PS Claim 6: Page 277-278; 290pp; Japanese.

XX This invention relates to an anti-attention deficit disorder or anti-
CC narcolepsy agent containing a polypeptide with a sequence identical or
CC substantially similar to a fully defined 12 amino acid sequence given in
CC the specification, and its amide, ester or their salt. The peptides
CC have ligand activity to sensory epithelium neuropeptide-like receptor
CC (SENR) protein. The invention also includes a method for diagnosing
CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
CC schizophrenia or fear. The polypeptides of the invention, their
CC precursor proteins and their encoding DNAs are useful in treating
CC attention deficit disorder or narcolepsy, or for screening drug
CC candidates for these indications and for anxiety, depression, insomnia,
CC schizophrenia or fear. They are also useful for gene therapy. The
CC polypeptide is a G protein-coupled receptor protein, with ligand
CC activity to sensor epithelium neuropeptide-like receptor. The present
CC sequence represents the rat sensory endothelium neuropeptide-like
CC receptor protein of the invention.

XX

Sequence 123 AA:

Query Match 100.0%; Score 633; DB 23; Length 123;
Best Local Similarity 100.0%; Pred. No. 5.8e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDRVPFCCLFVGLNPLSPVYDTGEMSLQLPVLEENMLRALELELRTALLQTLRQTV 60
DB 1 MDRVPFCCLFVGLNPLSPVYDTGEMSLQLPVLEENMLRALELELRTALLQTLRQTV 60
QY 61 GTEAEGSLGQADPSAETPTPRGSLRKALTGODSNTVLSRLLRTRKQKOGTAPECFWK 120
DB 61 GTEAEGSLGQADPSAETPTPRGSLRKALTGODSNTVLSRLLRTRKQKOGTAPECFWK 120
QY 121 YCI 123
DB 121 YCI 123

RESULT 4
AAY93647
ID AAY93647 standard; Protein: 123 AA.
XX
AC AAY93647;
XX
DT 25-SEP-2000 (first entry)
XX
DE Amino acid sequence of murine prepro-urotensin II (UII) polypeptide.
XX
KW urotensin II: motor neuron; hypertensive; neurodegeneration;
KW spinal cord trauma; hemi-plegia; para-plegia;
KW amyotrophic lateral sclerosis; antihypertensive agent.
XX
OS Mus sp.
XX
XX
XX Key Location/Qualifiers
FH 1..20
FT Peptide /note= "signal peptide"
FT 21..106
FT Peptide /note= "pro-segment"
FT 107..123
FT Peptide /note= "urotensin II"
PN WO200031265-A1.
XX
PD 02-JUN-2000.
XX

PF 26-NOV-1999; 99WO-FR02941.
XX
PR 26-NOV-1998; 98FR-0014914.
XX
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Beauvillain J, Coulouarn Y, Jegou S, Lohrmann I, Vaudry H;
XX
XX WPI: 2000-400075/34.
DR N-PSDB: AAA6719.
XX
PT New mammalian urotensin II polypeptide, useful for treating
PT neurodegeneration and spinal cord injury

PS Claim 2: Page 31; 42pp; French.

XX The present sequence represents a murine prepro-urotensin II polypeptide.
CC In mammals, urotensin II promotes survival and regeneration of motor
CC neurons, and also has a hypertensive effect. The urotensin II
CC polypeptides and polynucleotides are useful for treating
CC neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
CC para-plegia or amyotrophic lateral sclerosis). The polypeptides
CC are also used to screen for specific inhibitors, i.e. potential
CC antihypertensive agents.

XX

Sequence 123 AA:

Query Match 85.5%; Score 541; DB 21; Length 123;
Best Local Similarity 84.6%; Pred. No. 8.3e-52;
Matches 104; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDRVPFCCLFVGLNPLSPVYDTGEMSLQLPVLEENMLRALELELRTALLQTLRQTV 60
DB 1 MDRVPFCCLFVGLNPLSPVYDTGERTQLPVLLEDALRALELELRTALLQTLRQTM 60
QY 61 GTEAEGSLGQADPSAETPTPRGSLRKALTGODSNTVLSRLLRTRKQKOGTAPECFWK 120
DB 61 GTEAEGSPGEAGPSTPTPTPRGSMKAFAGONSNTVLSRLLRTRKQKOGTAPECFWK 120
QY 121 YCI 123
DB 121 YCI 123

RESULT 5
AAB60445
ID AAB60445 standard; Protein: 123 AA.
XX
AC AAB60445;
XX
DT 24-APR-2001 (first entry)
XX
DE Mouse urotensin II-like peptide precursor protein, SEQ ID NO:26.
XX
KW urotensin II-like peptide; precursor protein; mouse; murine; SENR ligand;
KW drug screening; sensory epithelium neuropeptide-like receptor;
KW diagnosis; central nervous function; cardiac function;
KW circulatory function.
XX
OS Mus sp.
XX
XX
XX WO200104298-A1.
XX
XX 18-JAN-2001.
XX
XX 06-JUL-2000; 2000WO-JP04484.
XX
XX 08-JUL-1999; 99JP-0194091.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Sugo T, Kurihara M, Kitada C, Mori M;
XX
XX

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XX  Beavuvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;
PI  WPI: 2000-400075/34.
DR  N-PSDB: AAA46710.
XX
XX  New mammalian urotensin II polypeptide, useful for treating
PT  neurodegeneration and spinal cord injury -
XX
XX  Disclosure: Page 30; 42pp: French.
PS
XX  The present sequence represents a rat prepro-urotensin II polypeptide.
CC  In mammals, urotensin II promotes survival and regeneration of motor
CC  neurons, and also has a hypertensive effect. The urotensin II
CC  polypeptides and polynucleotides are useful for treating
CC  neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
CC  para-plegia or amyotrophic lateral sclerosis). The polypeptides
CC  are also used to screen for specific inhibitors, i.e. potential
CC  antihypertensive agents.
XX
XX  Sequence 123 AA:
SQ
XX  Query Match 100.0%; Score 633; DB 21; Length 123;
XX  Best Local Similarity 100.0%; Pred. No. 5.8e-62;
XX  Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MDRVPCCLLFVGLNPLSFVYDTGEMSLQVLEENALRALEELERRALLQTLKQTV 60
DB 1 MDRVPCCLLFVGLNPLSFVYDTGEMSLQVLEENALRALEELERRALLQTLKQTV 60
XX
XX  61 GTEAEGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKORHGTAPCEFWK 120
QY 61 GTEAEGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKORHGTAPCEFWK 120
DB 61 GTEAEGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKORHGTAPCEFWK 120
XX
XX  121 YCI 123
QY 121 YCI 123
DB 121 YCI 123
XX
XX  RESULT 2
XX  AAB60442
XX  ID AAB60442 standard; Protein; 123 AA.
XX
XX  AAB60442;
XX
XX  24-APR-2001 (first entry)
DT
XX
XX  Rat urotensin II-like peptide precursor protein, SEQ ID NO:13.
DE
XX
XX  Urotensin II-like peptide; precursor protein; rat; SENR ligand;
KW  drug screening; sensory epithelium neuropeptide-like receptor;
KW  diagnosis; central nervous function; cardiac function;
KW  circulatory function.
XX
XX  Rattus sp.
OS
XX
XX  WO200104298-A1.
XX  PN
XX  18-JAN-2001.
XX  PD
XX  06-JUL-2000; 2000WO-JP04484.
XX  PF
XX  08-JUL-1999; 99JP-0194091.
XX  PR
XX  (TAKE ) TAKEDA CHEM IND LTD.
XX  PA
XX  Sugo T, Kurihara M, Kitada C, Mori M;
PI
XX  WPI: 2001-147192/15.
XX  DR
XX  N-PSDB: AAF59574.
XX  PT
XX  Urotensin II-like peptide originating in rat or mouse and encoded
XX  nucleic acid, useful in study of its physiological effects, for

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PT  diagnosis and development of drugs for controlling e.g. central nervous
PI  function -
XX
XX  Claim 5; Page 95; 110pp; Japanese.
PS
XX
XX  The invention relates to novel rat and mouse urotensin II-like peptide
CC  (AAB60443-AAB60444, AAB60445, AAB60446, AAB60447, AAB60448), their amides, esters
CC  or salts, their precursor proteins (AAB60442, AAB60443), and to nucleic
CC  acids encoding the urotensin II-like peptides (AAF59575-AAF59576,
CC  AAF59585-AAF59589) or the urotensin II-like peptide protein precursors
CC  (AAF59574, AAF59584). The urotensin II-like peptide are ligands of the
CC  sensory epithelium neuropeptide-like receptor (SENR). The invention also
CC  relates to vectors and transformants comprising the novel nucleic acid
CC  sequences, the recombinant production of the rat or mouse urotensin II-
CC  like peptides or their precursors, an antibody against a urotensin II-
CC  like peptide or precursor, a method of screening for compounds which can
CC  modulate the binding of urotensin II-like peptides to the SENR, the
CC  compounds thus identified, and a method of quantitating urotensin II-like
CC  peptides or their precursors. The peptides and proteins, and nucleic
CC  acids encoding them are useful in study of the physiological effects of
CC  urotensin II-like peptide/SENR interactions, and for the diagnosis and
CC  development of drugs (including gene therapy compositions) for modulating
CC  e.g., central nervous function, cardiac function and circulatory
CC  function. The present sequence represents the rat urotensin II-like
CC  peptide precursor protein of the invention.
XX
XX  Sequence 123 AA:
SQ
XX  Query Match 100.0%; Score 633; DB 22; Length 123;
XX  Best Local Similarity 100.0%; Pred. No. 5.8e-62;
XX  Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 MDRVPCCLLFVGLNPLSFVYDTGEMSLQVLEENALRALEELERRALLQTLKQTV 60
QY 1 MDRVPCCLLFVGLNPLSFVYDTGEMSLQVLEENALRALEELERRALLQTLKQTV 60
DB 1 MDRVPCCLLFVGLNPLSFVYDTGEMSLQVLEENALRALEELERRALLQTLKQTV 60
XX
XX  61 GTEAEGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKORHGTAPCEFWK 120
QY 61 GTEAEGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKORHGTAPCEFWK 120
DB 61 GTEAEGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKORHGTAPCEFWK 120
XX
XX  121 YCI 123
QY 121 YCI 123
DB 121 YCI 123
XX
XX  RESULT 3
XX  AA080121
XX  ID AA080121 standard; Protein; 123 AA.
XX
XX  AA080121;
XX
XX  07-OCT-2002 (first entry)
DT
XX
XX  Rat sensory epithelium neuropeptide-like receptor (SENR) protein.
DE
XX
XX  SENR: Sensory epithelium neuropeptide-like receptor; rat; fear;
KW  attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
KW  schizophrenia; G protein-coupled; receptor.
XX
XX  Rattus sp.
OS
XX
XX  WO200214513-A1.
XX  PN
XX  21-FEB-2002.
XX  PD
XX  10-AUG-2001; 2001WO-JP06899.
XX  PF
XX  10-AUG-2000; 2000JP-0247968.
XX  PR
XX  (TAKE ) TAKEDA CHEM IND LTD.
XX  PA
XX  Matsumoto Y, Watanabe T, Takahashi H, Mori M;
PI
XX

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DB 325 KTLAKLALSDPN--KSHLLESTYM-LKRREIDEC 355

RESULT 13

09ZMB6 PRELIMINARY: PRT: 534 AA.

AC 09ZMB6; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

GN F21M11.11 protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;

RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,

RA Altati H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,

RA Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,

RA Lueros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,

RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC003027; AAD10674.1;

DR InterPro: IPR002048; EF-hand.

DR Pfam: PF00036; ehand.1.

DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.

SQ SEQUENCE 534 AA: 61847 MW: 404573626579196 CRC64;

Query Match

Best Local Similarity 26.0%; Score 74.5; DB 10; Length 534;

Matches 27; Conservative 21; Mismatches 33; Indels 23; Gaps 4;

QY 23 LLDSEISF---QLSAPHEARLTPPELERASLLQILPEMLGAERGI-----LKRADS 73

DB 405 VITSNEMQFFEEQOL---HMECTIQEAVLFSDILCOIIMIPKENCITLDDKSKL 461

QY 74 STINFPRGMLRKRFQDSGDPNILLSHLLARIWKPKKRETPD 117

DB 462 SANVFNILLFNLKFMFETRDPELI-----RQEREDPN 494

RESULT 14

098RS6 PRELIMINARY: PRT: 827 AA.

AC 098RS6; 01-OCT-2001 (TREMBlrel. 18, Created)

DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)

DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)

DE US small nuclear ribonucleoprotein 116 kDa subunit.

GN 55 SNRP.

OS Guillardia theta (Cryptomonas phi).

OC Nucleomorph.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.

OX NCBI_TaxID=55529;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=21233349; PubMed=11323671;

RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,

RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;

RT "The highly reduced genome of an enslaved algal nucleus.;"

RL Nature 410:1091-1096(2001).

DR EMBL: AF165818; AAK39871.1;

DR InterPro: IPR000795; EF_GTPbind.

DR InterPro: IPR001810; F-box.

DR Pfam: PF00009; GTP_EFTU; 1.

DR PRINTS: PR00315; ELONGATNCT.

DR PROSITE: PS50181; FBOX; 1.

KM GTP-binding; Nucleocapsid; Protein biosynthesis; Ribonucleoprotein.

SQ SEQUENCE 827 AA: 96891 MW: 4FAEL0A0DB93DOA3 CRC64;

Query Match

Best Local Similarity 11.4%; Score 74.5; DB 8; Length 827;

Matches 26; Conservative 16; Mismatches 30; Indels 21; Gaps 5;

QY 39 DARLTPPELERASLLQILPEMLGAERGIILRK---ADSSNTINP-----RGNL 84

DB 192 ELKMTDPEVOK-RILQILDELNYLALHKYINKSVLSKRNINFPNLDNVCFSALSGWL 250

QY 85 RKFDPSG---QDPNILLSH--LLARIWKPKY 111

DB 251 FNLNPSGLYMIISOPSTLSQKDLSEKRWMDK 283

RESULT 15

08VZC7 PRELIMINARY: PRT: 1202 AA.

AC 08VZC7; 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DE AF5945510/MRC19_18.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

RA Bowser L., Carlini P., Chang E., Dale J.M., Goldsmith A.D.,

RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlín-Neumann G.,

RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,

RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,

RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,

RA Ecker J.R.;

RT "Arabidopsis cDNA clones.;"

RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY065063; AAL57696.1;

DR InterPro: IPR001611; LRR.

DR Pfam: PF00560; LRR; 5.

SQ SEQUENCE 1202 AA: 135815 MW: 15F84681326E9DA CRC64;

Query Match

Best Local Similarity 28.6%; Score 74.5; DB 10; Length 1202;

Matches 26; Conservative 19; Mismatches 25; Indels 21; Gaps 5;

QY 30 SFQLSAPHEARLTPPELERASLLQILPEMLGAERGILKKAADSTINFPNGMLRKRFQD 89

DB 398 SYKLNKDEE-RLIKETEM-----VLSAERGN--PSDSESSSPK-----K 437

QY 90 FSGODPNILLSHLLARIWKPKKRETPDCF 120

DB 438 ASGENPILLAYKILFTDGPLKD-TIIDCFW 467

Search completed: March 10, 2003, 17:46:33

Job time : 26.7946 secs

DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 392 AA; 46122 MW; D5C3DC359083A350 CRC64;

Query Match 11.8%; Score 77; DB 17; Length 392;
 Best Local Similarity 24.1%; Pred. No. 8.8;
 Matches 26; Conservative 25; Mismatches 31; Indels 26; Gaps 6;

OY 12 IGFNLPLSLPLDLSREISFQLSAPHEADRLPPEELERASLLQILPEMGAERGDLIRKA 71
 DB 274 IFLKELLIKIRKQGRKKLME---HESC---GQDLKRA-----MPLKGLIKDK 318
 OY 72 DSSTNIFNRGNLRKRFQD-----FSGDPNILLSHLARI-WKPYK 111
 DB 319 NKHFVL---GDLRFAEQMADIKMWDTSKNKYLILHNSSVDMQHYK 363

RESULT 10
 O9YA06 PRELIMINARY: PRT; 433 AA.

AC O9YA06; 01-NOV-1999 (TRENBLREL. 12, Created)
 DT 01-NOV-1999 (TRENBLREL. 12, Last sequence update)
 DE 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
 GN APEI887.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
 OC Desulfurococcaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RA MEDLINE=99310339; PubMed=10382966;
 RA Kavarabayasli Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jinno K., Takehashi M., Sekine M., Baba S.-I., Anai A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
 RA Yamazaki Y., Kushiida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000062; BAA80892.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 433 AA; 46766 MW; 2F0EF190D5EDD5B2 CRC64;

Query Match 11.7%; Score 76.5; DB 17; Length 433;
 Best Local Similarity 29.5%; Pred. No. 11;
 Matches 33; Conservative 13; Mismatches 29; Indels 37; Gaps 7;

OY 23 LIDSREISFQLSAPHEADRLPPEELERASLLQILPEMGAERGDLIRKA 71
 DB 171 LVSSR-----AMHEDLARLGLVELVDPDEFARYVAESVPEISGEEVLRRGEVLDA 223
 OY 72 DSSTNIFNRGNLRKRFQDPSGDPNILLSHLARIWKPY-KKREPPDCFWKY 122
 DB 224 DG-----EKKSLRYR-----AIKRMKSRGLDAVSPACWIFY 257

RESULT 11
 O9AW95 PRELIMINARY: PRT; 608 AA.

AC O9AW95; 01-JUN-2001 (TRENBLREL. 17, Created)
 DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
 DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 GN Anthranilate synthase alpha subunit (EC 4.1.3.27).
 OS Asa.
 OC Catharanthus roseus (Röy periwinkle) (Madagascar periwinkle).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfiaceae;

OC Vinnecae; Catharanthus.
 OX NCBI_TaxID=4058;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Q.DON; TISSUE=CELL SUSPENSION;
 RA Bongaearts R.J.M., Meijer A.H., Hoge J.H.C., Verpoorte R.;
 RT "Molecular cloning and characterization of a cDNA clone encoding the
 RT alpha-subunit of the enzyme anthranilate synthase from Catharanthus
 RT roseus.";
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250008; CAC29060.1; -
 DR HSP; Q06128; 1QDL.
 DR InterPro: IPR005256; Anth_synth.
 DR InterPro: IPR005350; Chorismate_bind.
 DR Pfam: PF00425; Chorismate_bind.
 DR PRINTS: PR00095; ANTSNTASEI.
 DR ProDom: PD000779; Chorismate_bind; 1.
 DR TIGRfams: TIGR00564; trpE_most; 1.
 KW Lyase.
 SQ SEQUENCE 608 AA; 68263 MW; DEE052CE5A1FC15E CRC64;

Query Match 11.6%; Score 76; DB 10; Length 608;
 Best Local Similarity 20.8%; Pred. No. 20;
 Matches 35; Conservative 28; Mismatches 41; Indels 64; Gaps 9;

OY 2 YKLASCLLFIQFLNPLSLPLD-----SREISFQLSAPH----- 37
 DB 49 FRLACCSLHL-----LVLSPLDLKCSAVSPSFVDSAKFKVAKHGNLILYRPIFS 104
 OY 38 -----EDARLTP-----EEL-----RASLIQILPEMGAERGDLIRKA 71
 DB 105 HLPVLAAYCLVKEDDREAPSFLESVEPGLKAVNGRVSVIGAQPTM-----EIVAKE 158

OY 72 DSSTNIFNRGNLRKRFQDPSGDPNILLSHLARIWKPYKKREPPDCF 119
 DB 159 NMVYVDHROG--RVEQYE-EDPMVVPRIEMK-WKPORTTELPAPAF 202

RESULT 12
 O9LVB5 PRELIMINARY: PRT; 461 AA.

AC O9LVB5; 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DE 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
 GN Genomic DNA, chromosome 5, YAC clone:K14A3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI";
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB025609; BAA98109.1; -
 DR InterPro: IPR000679; Znf_GATV.
 DR Pfam: PF00320; GATV; 1.
 DR SMART: SM00401; Znf_GATV; 1.
 SQ SEQUENCE 461 AA; 51682 MW; 49FD67D43F3D52DC CRC64;

Query Match 11.5%; Score 75; DB 10; Length 461;
 Best Local Similarity 26.6%; Pred. No. 18;
 Matches 25; Conservative 13; Mismatches 32; Indels 24; Gaps 4;

OY 46 ELERASLLQILPEMGAERGDLIRKADST-----NIFNRGNLRKRFQD 90
 DB 265 EEEQOKLMLLQOVDSVDPDPSLRSMFESSQREKNSLFLQOLVADGVFTNSYAKLEDI 324
 OY 91 SG-----ODPNILLSHLARIWKPYKKREPPDC 118


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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fjosek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshell A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -I- SIMILARITY: CONTAINS 1 SET DOMAIN.
DR EMBL: AF003704; AAF55041.2; -.
DR HSSP: P20393; IABY.
DR FlyBase: FBgn0003862; trx.
DR InterPro: IPR003889; FYrich.C.
DR InterPro: IPR003888; FYrich.N.
DR InterPro: IPR003616; PostSET.
DR InterPro: IPR001214; SET.
DR InterPro: IPR001965; ZnF_PHD.
DR InterPro: IPR001841; ZnF_Ring.
DR Pfam: PF00628; PHD; 3.
DR Pfam: PF00856; SET; 1.
DR SMART: SM00542; FYRC; 1.
DR SMART: SM00541; FYRN; 1.
DR SMART: SM00249; PHD; 4.
DR SMART: SM00508; PostSET; 1.
DR SMART: SM00184; RING; 3.
DR SMART: SM00317; SET; 1.
DR PROSITE: PSS0280; SET; 1.
SQ SEQUENCE 3726 AA; 400095 MW; E3DDB8F062BD796 CRC64;

Query Match 12.1%; Score 79; DB 5; Length 3726;
Best local Similarity 30.0%; Pred. No. 95;
Matches 24; Conservative 12; Mismatches 28; Indels 16; Gaps 3;

OY 29 ISFQSLAPHEADARLPEELERASLLQILPEMLGAERGLIRKADSSNIIFNPGNRKFKQ 88
DB 857 ISFQLDPAH-----RSRLSAILPPGM---KGAARAEKSAELSLPSGSRFTS 902
OY 89 DRFGQDPNILLSHLARIMK 108
DB 903 TASSSSPVSVASTSVK--WK 920

RESULT 8
OYXSL4 PRELIMINARY; PRT; 364 AA.
ID OYXSL4;
AC OYXSL4;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE MHC class I antigen (Fragment).
OS Aulonocara hansbaenschii.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;

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OC Cichlidae; Aulonocara.
OX NCBI_TaxID=27781;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=97293242; Pubmed=9148790;
RA Sato A., Klein D., Sultman H., Figueroa F., O'Huigin C., Klein J.;
RT "Class I MHC genes of cichlid fishes: identification, expression, and
RT polymorphism.";
RL Immunogenetics 46:63-72(1997).
CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
CC IMMUNE SYSTEM (BY SIMILARITY).
CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
CC MICROGLOBULIN) (BY SIMILARITY).
DR EMBL: AF038551; AAD37814.1; -.
DR InterPro: IPR003597; I9-cl.
DR InterPro: IPR003006; I9_MHC.
DR InterPro: IPR001039; MHC_I.
DR Pfam: PF00047; I9; 1.
DR Pfam: PF00129; MHC_I; 1.
DR PRINTS: PR01638; MHCCLASSI.
DR PRODOM: PD000050; MHC_I; 1.
DR SMART: SM00407; IGCL; 1.
KW Glycoprotein; Transmembrane.
FT NON_TER 364
SQ SEQUENCE 364 AA; 41428 MW; 051914ED23D3CB8F CRC64;

Query Match 11.8%; Score 77; DB 7; Length 364;
Best local Similarity 29.1%; Pred. No. 8;
Matches 30; Conservative 21; Mismatches 36; Indels 16; Gaps 4;

OY 23 LIDREISFQSLAPHEADARLPEELERASLLQILPEMLGAERGLIRKADSSNIIFNPGR 82
DB 248 ILRNNDDTFQMSYDLKLSDTPEEMER---YDCVFHLSGE--DIYKRLNALIRTNPEG 302
OY 83 NLRRFQDFSGQDPNILLSHLA-----RIKKYKRRKT 115
DB 303 NLRR-ETPSSGLISITIASVVALILVAVGAVAKKKKKRRKT 344

RESULT 9
OYXSL4 PRELIMINARY; PRT; 392 AA.
ID OYXSL4;
AC OYXSL4;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein AF2358.
GN AF2358.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; Pubmed=9389475;
RA Klek H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson R.D., Kierlavage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftis B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL: AE001113; AAB91305.1; -.
DR TIGR: AF2358; -.
DR InterPro: IPR003662; sub_transporter.

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RP SEQUENCE FROM N.A.
RA Bevan M., Tertyn N., Ardiles W., Buysshaert C., Dasseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Gielen J., Van Montagu M., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.,
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL162973; CAB86047.1;
DR InterPro: IPR001810; F-box.
DR Pfam: PF00646; F-box; 1.
DR SMART: SM00256; FBOX; 1.
DR PROSITE: PS0181; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE: 469 AA; 53949 MW; 4113E6184A447C8E CRC64;

Query Match          12.1%; Score 79.5; DB 10; Length 469;
Best Local Similarity 26.1%; Pred. No. 6.1;
Matches 35; Conservative 21; Mismatches 51; Indels 27; Gaps 5;

OY 4 LASCOLLIGFLNPLLSPLDLSREISFOLSAFH---EDARLTPPELERASLQ--ILP 57
DB 176 LFDCTMSDESEFLEILSGCPILSLSLKFCOMSLKYLNLKSLRLTLRLTERISYINAPMLS 235
OY 58 EMLAERGDILFRKADS-----STNIFNPGNLKRFQDFSCODPNILLS 100
DB 236 MOIVAPYHILRLRSEAHCFVDVSVSLTEANVDSTFHR---TCYHDFDLDPHDLIV 292
OY 101 HLLARIMPKYKRR 114
DB 293 -MVGTMKTFKVE 305

RESULT 6
O9W2R1 PRELIMINARY; PRT; 543 AA.
ID 09W2R1
AC 09W2R1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE CG9993 protein.
GN CG9993.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abirl J.F., Abmayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cusum S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harits N.L., Harey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mcherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003452; AAF46629.1;
DR HSSP: P08659; IIC1.
DR FlyBase: FBgn0034553; CG9993.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR000508; Signatase.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE: PS00761; SPASE_13; 1.
SQ SEQUENCE: 543 AA; 60344 MW; A6A9B06E1457DCF9 CRC64;

Query Match          12.1%; Score 79.5; DB 5; Length 543;
Best Local Similarity 28.2%; Pred. No. 7.3;
Matches 40; Conservative 15; Mismatches 42; Indels 45; Gaps 9;

OY 23 LIDSREISFOLSAFHEDARL--TPPELERASLQI-----LPEMLGA 62
DB 271 LVERHQVSEFLVPHHMLAKSPERQELAAKQCQVSCSKVPMGIMQLYELLA 330
OY 63 ERGDIL----RKADSTNIFNPGN---LRKFGQ---DFSGOD--PNLLSHLLARI-- 106
DB 331 NFEAVLYLGTETGSLKNGVGLSGRLLRVQRVVPDHCQSLGN--QTQQLIVRLNL 389
OY 107 -WKPY-----KKRTPDPCFW 120
DB 390 RWGCVHNPQETGVYTPDCKW 411

RESULT 7
O9VFL1 PRELIMINARY; PRT; 3726 AA.
ID 09VFL1
AC 09VFL1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Trx protein.
GN Trx OR CG8651.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abirl J.F., Abmayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,

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DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Urotensin II transcript variant 1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Mori M., Sugo T., Abe M., Shimomura Y., Kurihara M., Kitada C.,
RA Kikuchi K., Shintani Y., Kurokawa T., Onda H., Nishimura O.,
RA Fujino M.;
RT "Urotensin II is the endogenous ligand of a G-protein-coupled orphan
RT receptor, SENR (GPR14).";
RL Biochem. Biophys. Res. Commun. 265:123-129(1999).
DR EMBL: AB063245; BAB60888.1; -
DR EMBL: AB063244; BAB60887.1; -
DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II.
DR PROSITE: PS00984; UROTENSIN_II; UNKNOWN_1.
SQ SEQUENCE 121 AA; 13580 MW; 656E4B01AF69101B CRC64;

Query Match
Best Local Similarity 52.3%; Score 342.5; DB 6; Length 121;
Matches 77; Conservative 12; Mismatches 31; Indels 5; Gaps 4;

QY 1 MYKLASCLLFGLFGLNPLSLPLDSREISFQLSAPHEDARLTPELEASLIQILPEML 60
DB 1 MSKLVP-CLLLGCLGLFALPVPDSRKPELPFSAP-EDVRSAMDELRASLIQILPELP 58
QY 61 GAERGDILRKADSTNIFNPGNLKRFQDFSGODPNILSHLARIMKPYKKREP-DCF 119
DB 59 GAEAGEDLRADAGMDITFPGEMRK--AFSGODPNIFLSHLARIMKPYKKRGPSECF 116
QY 120 WKYCV 124
DB 117 WKYCV 121

RESULT 3
Q95K72 PRELIMINARY; PRT; 85 AA.
AC Q95K72;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Urotensin II transcript variant 2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Mori M., Sugo T., Abe M., Shimomura Y., Kurihara M., Kitada C.,
RA Kikuchi K., Shintani Y., Kurokawa T., Onda H., Nishimura O.,
RA Fujino M.;
RT "Urotensin II is the endogenous ligand of a G-protein-coupled orphan
RT receptor, SENR (GPR14).";
RL Biochem. Biophys. Res. Commun. 265:123-129(1999).
DR EMBL: AB063246; BAB60889.1; -

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DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II.1.
DR PROSITE: PS00984; UROTENSIN_II; UNKNOWN_1.
SQ SEQUENCE 85 AA; 9644 MW; F519CFEDFCBA863 CRC64;

Query Match
Best Local Similarity 32.9%; Score 215.5; DB 6; Length 85;
Matches 53; Conservative 10; Mismatches 21; Indels 41; Gaps 4;

QY 1 MYKLASCLLFGLFGLNPLSLPLDSREISFQLSAPHEDARLTPELEASLIQILPEML 60
DB 1 MSKLVP-CLLLGCLGLFALPVPDSRK----- 27
QY 61 GAERGDILRKADSTNIFNPGNLKRFQDFSGODPNILSHLARIMKPYKKREP-DCF 119
DB 28 -----EPLPFSAGMDITFPGEMRK--AFSGODPNIFLSHLARIMKPYKKRGPSECF 80
QY 120 WKYCV 124
DB 81 WKYCV 85

RESULT 4
Q47972 PRELIMINARY; PRT; 140 AA.
AC Q47972;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, last annotation update)
DE B1P protein.
GN B1P.
OS Halobacterium salinarum.
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=2242;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL;
RA Gropp F., Gropp R., Betlach M.C.;
RT "The fourth gene in the hop gene cluster is co-regulated with the hop
RT gene.";
RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: L22007; AAD15050.1; -
SQ SEQUENCE 140 AA; 15516 MW; 8C14F71C32867641 CRC64;

Query Match
Best Local Similarity 12.2%; Score 80; DB 1; Length 140;
Matches 21; Conservative 16; Mismatches 27; Indels 8; Gaps 1;

QY 43 TPPELEASLIQILPEMLGAERGDILRKADSTNIFNPGNLKRFQDFSGODPNILSHL 102
DB 63 TVEDIERVQRRLVQELTGALDITTYRLSTRTHVADLRGRVRL-----PTVIESV 114
QY 103 LARIWKPKYKRE 114
DB 115 LAPIAKAYMKRE 126

RESULT 5
Q9LYZ2 PRELIMINARY; PRT; 469 AA.
AC Q9LYZ2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE Hypothetical 53.9 kDa protein.
GN F9G14_240.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:35:28 ; Search time 23.7946 seconds

(without alignments)
1073.767 Million cell updates/sec

Title: US-09-831-907A-1

Perfect score: 655
Sequence: 1 MYKLASCCLLFTGFLNPLLS.....RIWKPKKRETPDCFWKVCV 124

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	577	88.1	139	4	Q8TAU6	Q8tau6 homo sapien
2	342.5	52.3	121	6	Q95J46	Q95j46 sus scrofa
3	215.5	32.9	85	6	Q95K72	Q95k72 sus scrofa
4	80	12.2	140	1	Q47972	Q47972 halobacteri
5	79.5	12.1	469	10	Q9LYZ2	Q9lyz2 arabidopsis
6	79.5	12.1	543	5	Q9W2R1	Q9w2r1 drosophila
7	79.5	12.1	3726	5	Q9VFL1	Q9vfl1 drosophila
8	77	11.8	364	7	Q9XSI4	Q9xsi4 aulonocara
9	77	11.8	392	17	Q30312	Q30312 archaeglob
10	76.5	11.7	433	17	Q9YAO6	Q9yao6 aetopyrum p
11	76	11.6	608	10	Q9AW95	Q9aw95 catenanthu
12	75	11.5	461	10	Q9L7B5	Q9l7b5 arabidopsis
13	74.5	11.4	534	10	Q9ZWB6	Q9zwb6 arabidopsis
14	74.5	11.4	827	8	Q9HRS6	Q9hrs6 guillardia
15	74.5	11.4	1202	10	Q8VZC7	Q8vzc7 arabidopsis
16	74.5	11.4	1214	10	Q9FHI5	Q9fhi5 arabidopsis

17	73	11.1	256	16	Q9Z7L3	Q9z7l3 chlamydia p
18	73	11.1	814	4	Q9Y5C7	Q9y5c7 homo sapien
19	73	11.1	929	4	Q9Y5G1	Q9y5g1 homo sapien
20	72.5	11.1	134	3	P79028	P79028 emeritella
21	72.5	11.1	557	5	Q17948	Q17948 caenorhabd1
22	72.5	11.1	561	5	Q9U301	Q9u3q1 caenorhabd1
23	72	11.0	465	5	Q9GW58	Q9gn58 drosophila
24	72	11.0	465	5	Q9GTU4	Q9gtu4 drosophila
25	71.5	10.9	175	12	Q9YS19	Q9ys19 rotavirus a
26	71	10.8	381	5	Q19458	Q19458 caenorhabd1
27	70.5	10.8	287	10	Q9SBD4	Q9sbd4 arabidopsis
28	70.5	10.8	321	10	Q04258	Q04258 arabidopsis
29	70.5	10.8	323	10	Q9SMH4	Q9smh4 arabidopsis
30	70.5	10.8	411	10	Q9SKG3	Q9skg3 arabidopsis
31	70.5	10.8	411	10	Q9S8B3	Q9s8b3 arabidopsis
32	70.5	10.8	1094	12	P89680	P89680 lobacaco str
33	70.5	10.8	1131	16	Q8V743	Q8v743 anabaena sp
34	70	10.7	495	10	Q8RWT1	Q8rwt1 arabidopsis
35	70	10.7	815	10	Q9FZ65	Q9fz65 arabidopsis
36	69.5	10.6	336	10	Q9SZ00	Q9sz00 mycobacteri
37	69.5	10.6	359	3	Q42836	Q42836 sordaria ma
38	69.5	10.6	802	4	Q9UQ37	Q9uq37 homo sapien
39	69.5	10.6	1262	4	Q9UQ40	Q9uq40 homo sapien
40	69.5	10.6	1783	4	Q15038	Q15038 homo sapien
41	69.5	10.6	1791	4	Q60382	Q60382 homo sapien
42	69.5	10.6	2296	4	Q9UHA8	Q9uha8 homo sapien
43	69.5	10.6	2752	4	Q9UQ35	Q9uq35 homo sapien
44	69.5	10.6	82	11	Q9CTF4	Q9ctf4 mus musculu
45	69	10.5				

ALIGNMENTS

RESULT 1
ID Q8TAU6 PRELIMINARY: PRT: 139 AA.
AC Q8TAU6.
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to urolensln 2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PANCREAS;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025776; AAH25776.1; -
SQ SEQUENCE 139 AA: 16276 MW: 32DC52936D5BDB6 CRC64:

Query Match 88.1%; Score 577; DB 4; Length 139;
Best Local Similarity 99.1%; Pred. No. 1.1e-52;
Matches 112; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MYKLASCCLLFTGFLNPLLSPLTDSREISFQLSAPHEHARLPPELEERASLQILPEML	60
DB	1	MYKLASCCLLFTGFLNPLLSPLTDSREISFQLSAPHEHARLPPELEERASLQILPEML	60
QY	61	GARGDILRKADSSSTNFNRGNLRRKQDFSGODPNILSLHLARLWKPKKR	113
DB	61	GARGDILRKADSSSTNFNRGNLRRKQDFSGODPNILSLHLARLWKPKKR	113
RESULT 2			
ID Q95J46	PRELIMINARY:	PRT:	121 AA.
AC Q95J46;			
DT 01-DEC-2001 (TREMBlrel. 19, Created)			
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)			

Tue Mar 11 10:10:15 2003

Search completed: March 10, 2003, 17:39:19
Job time : 9.03784 secs

us-09-831-907a-1.rsp

FT CHAIN 293 431 BONE MORPHOGENETIC PROTEIN 7.
 FT DISULFID 330 396
 FT DISULFID 359 428
 FT DISULFID 363 430
 FT DISULFID 385 385
 FT CARBOHYD 187 187 INTERCHAIN.
 FT CARBOHYD 302 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 431 AA; 49313 MW; 47A05E45C6815F8A CRC64;

Query Match 10.5%; Score 69; DB 1: Length 431;
 Best Local Similarity 25.2%; Pred. No. 11;
 Matches 34; Conservative 15; Mismatches 50; Indels 36; Gaps 5;

QY 22 PLDSEISFQLSAPHEDARLPEELE-----RASLQILPEMLG----- 61
 DB 149 PRYHREFRDLISKIPEGEAVTAEPRIYKDYIRERFDNETFRISYQVQLGHLGRES 208
 QY 62 -----AERGDILRKADSSIN--IFNPRGNL--RKQDFSCODPILLSHLART 106
 DB 209 FLDDSTLMASEGWLVPFDTATSNHVVNPRNLGLQSLVETLDQSSINPKLAGLIGR- 267
 QY 107 WKPKKREPPDCFWK 121
 DB 268 HGPQNKQPFMWAFKK 282

RESULT 12
 NCAP_RINDL

ID NCAP_RINDL STANDARD: PRT; 525 AA.
 AC P37708;
 DT 01-OCT-1994 (Rel. 30; Created)
 DT 01-OCT-1994 (Rel. 30; Last sequence update)
 DT 01-OCT-1994 (Rel. 30; Last annotation update)
 DE Nucleocapsid protein.
 OS N.
 OS Rinderpest virus (strain L) (RDV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
 OX NCBI_TaxID=11243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91205763; PubMed=2017875;
 RA Kamata H., Tsukiyama K., Sugiyama M., Kamata Y., Yoshikawa Y.,
 RA Yamanouchi K.;
 RT "Nucleotide sequence of cDNA to the rinderpest virus mRNA encoding
 RT the nucleocapsid protein.";
 RL Virus Genes 5:5-15(1991).
 CC -!- FUNCTION: MOST ABUNDANT PROTEIN IN THE VIRION AND AN IMPORTANT
 CC ELEMENT CONFERRING HELICAL SYMMETRY ON THE NUCLEOPROTEIN CORE AS
 CC WELL AS INTERACTING WITH M PROTEIN DURING VIRION FORMATION.
 CC -!- SIMILARITY: BELONGS TO THE PARAMYXOVIRUSES NUCLEOCAPSID FAMILY.
 DR InterPro: IPR002021; Paramyx_ncap.
 DR Pfam: PF00973; Paramyx_ncap; 1.
 KW Nucleocapsid.
 SQ SEQUENCE 525 AA; 58131 MW; 582B8E6CA2AAC71F CRC64;

Query Match 10.5%; Score 69; DB 1: Length 525;
 Best Local Similarity 26.6%; Pred. No. 14;
 Matches 37; Conservative 20; Mismatches 56; Indels 26; Gaps 7;

QY 3 KLASCLLFLGFLNPLSLPLDSREIS----FQLSAPHEDARLPEELERASLQILPE 58
 DB 50 RLDDCLVKNWG--DPIISGPKLGTALISLIFVESFGQLIQRIIDDPDISIKLIVEIQS 107
 QY 59 -----MLGARGDIL--RKADSSINIFNPRG-----NLKKFQDFSGQDP---NIIL 99
 DB 108 DKYQSGILTRASKASMDDEADRFYTDPEPGEEROSYFENREIODIEVQDEGEFMIL 167
 QY 100 SHLLARIWKPKRR-ETPD 117
 DB 168 ATILAQIWLILAKAVYTPD 186

RESULT 13

ID DGLA_DEIRA STANDARD: PRT; 373 AA.
 AC O9RVM1;
 DT 15-JUN-2002 (Rel. 41; Created)
 DT 15-JUN-2002 (Rel. 41; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Deoxyguanosinetriphosphate triphosphohydrolase-like protein 1.
 GN DRI006.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus..
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RL;

RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans RL.";
 RL Science 286:1571-1577(1999)
 CC -!- SIMILARITY: BELONGS TO THE DGPASE FAMILY. SUBFAMILY 2.
 CC -!- SIMILARITY: BELONGS TO THE DGPASE FAMILY. SUBFAMILY 2.

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DR EMBL: AE001952; AAF10581.1; -.
 DR TIGR: DRI006;
 DR InterPro: IPR002819; HD.
 DR InterPro: IPR003607; ME_Plpase_HDC.
 DR Pfam: PF01966; HD; 1.
 DR SMART: SM00471; HDC; 1.
 KW Hypothetical protein; Hydrolase; Complete proteome.
 SQ SEQUENCE 373 AA; 41372 MW; 21DOA09B9BC6571 CRC64;

Query Match 10.5%; Score 68.5; DB 1: Length 373;
 Best Local Similarity 27.1%; Pred. No. 11;
 Matches 32; Conservative 16; Mismatches 31; Indels 39; Gaps 6;

QY 13 GLFNP--LASTPLDSEISFQLSAPHEDARLPEELERASLQILPEMLGARGDILRK 70
 DB 209 GLHPELDLEPLM--REL-----QERSGVTSQRPSSADLTQIRELLGMLIGDITRS 259

QY 71 AD---SSTNIENP-----RGNLRKFQDFSGQDPNILLSHLARIWK 108
 DB 260 SDAIAASGASPDVAQVAHNRVLTYSPLRGLHRCAGDE-----LBERLYRMQ 309

RESULT 14

GNTP_ZYMMO
 ID GNTP_ZYMMO STANDARD: PRT; 451 AA.
 AC O92670;
 DT 30-MAY-2000 (Rel. 39; Created)
 DT 30-MAY-2000 (Rel. 39; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Glucanate permease.
 GN GNTP.
 OS Zymomonas mobilis.
 OC Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 OC Zymomonas.

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RL Nature 417:141-147(2002).
CC -1- CATALYTIC ACTIVITY: (S)-malate + NAD(+) -> oxaloacetate + NADH.
CC -1- SIMILARITY: BELONGS TO THE LDH FAMILY. MDH SUPRANILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AL389898: CAB97430.1; -.
DR HSPSP: P10584; 1BDN.
DR InterPro: IPR001252; Mdh.
DR InterPro: IPR001236; 1dh.
DR Pfam: PF00056; 1dh; 1.
DR Pfam: PF02866; 1dh; 1.
DR ProDom: PD003052; Mdh; 1.
DR ProSITE: PS00068; MDH; 1.
DR Oxidoreductase: Tricarboxylic acid cycle; NAD; Complete proteome.
KW ACT_SITE 160 160 PROTON-RELAY (BY SIMILARITY).
FT BINDING 163 163 SUBSTRATE CARBOXYL GROUP (BY SIMILARITY).
FT ACT_SITE 188 188 PROTON-RELAY (BY SIMILARITY).
SQ SEQUENCE 329 AA; 34643 MW; 7653F74769CCAF4 CRC64;

Query Match 10.7%; Score 70; DB 1; Length 329;
Best Local Similarity 27.5%; Pred. No. 6.4;
Matches 22; Conservative 15; Mismatches 31; Indels 12; Gaps 3;

Oy 20 SUPPLDREISFOLSAHPEDARLTPELEBASLLOLPEMLGENDILRKADSTNIFN 79
Db 62 APFLLOGEIT-----DDPNVAFDGANVALLVGARPRKEMERDGL---EANGCIRK 111
Oy 80 PRGNLRKFDGFCGDPNILL 99
Db 112 POG--KAINDHADIKVLV 129

RESULT 11
BMP7_HUMAN STANDARD; PRT; 431 AA.
AC P18075; O9NTQ7; O9H512;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bone morphogenetic protein 7 precursor (BMP-7) (osteogenic protein 1)
DE (OP-1).
GN BMP7 OR OP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=placenta;
RX MEDLINE=90291971; PubMed=2357959;
RA Oezkaynak E., Rueger D.C., Drier E.A., Corbett C., Ridge R.J.,
RA Sampath T.K., Oppermann H.;
RT "OP-1 cDNA encodes an osteogenic protein in the TGF-beta family.";
RL EMBL J. 9:2085-2093(1990).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=91088608; PubMed=2263636;
RA Celeste A.J., Iannazzi J.A., Taylor R.C., Hewick R.M., Rosen V.,
RA Wang E.A., Wozney J.M.;
RT "Identification of transforming growth factor beta family members
RT present in bone-inductive protein purified from bovine bone.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9843-9847(1990).
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

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```

RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Dearden R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahman D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Leivasalho M.H., Leverisa M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McEay K., McMurtry A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prithaliam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sena H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Way P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
RN 14
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 293-431.
RX MEDLINE=96149402; PubMed=8570652;
RA Griffith D.L., Keck P.C., Sampath T.K., Rueger D.C., Carlson W.D.;
RT "Three-dimensional structure of recombinant human osteogenic protein
RT 1: structural paradigm for the transforming growth factor beta
RT superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:878-883(1996).
CC -1- FUNCTION: INDUCES CARTILAGE AND BONE FORMATION. MAY BE THE
CC OSTEOINDUCTIVE FACTOR RESPONSIBLE FOR THE PHENOMENON OF
CC EPITHELIAL OSTEOGENESIS. PLAYS A ROLE IN CALCIUM REGULATION
CC AND BONE HOMEOSTASIS.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE KIDNEYS AND BLADDER. LOWER
CC LEVELS SEEN IN THE BRAIN.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL: X51801; CAA36100.1; -.
DR EMBL: M60316; AAA36738.1; -.
DR EMBL: AL122058; CAB90273.1; -.
DR EMBL: AL157414; CAC08434.1; -.
DR PIR: S10529; S10529.
DR PIR: C39263; C39263.
DR PDB: 1BMP; 23-JUL-97.
DR Gene: HGNC:1074; BMP7.
DR MIM: 112267; -.
DR InterPro: IPR002400; GF_cysknoc.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 2.
DR Pfam: PF00688; TGFb-Propeptide; 2.
DR PRINTS: PR00438; GFCYSKNOT.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR ProSITE: PS00250; TGF_BETA_1; 1.
KW Signal; Growth factor; Cytokine; Bone; Cartilage; Glycoprotein;
KW 3D-structure.
FT SIGNAL 1 29 POTENTIAL.
FT PROPEP 30 292 POTENTIAL.

```


RT "Contrasting molecular population genetics of four hexokinases in
RT Drosophila melanogaster and Drosophila simulans."
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-Oregon-K:
RA Deobagkar D.D., Kulkarni G.V., Deobagkar D.N.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN-Berkeley:
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gliedok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkllov G., Mlshina N.V., Mobarly C., Morris J., Mostreit A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -|- CATALYTIC ACTIVITY: ATP + D-hexose = ADP + D-hexose 6-phosphate.
CC -|- PATHWAY: FIRST STEP OF SEVERAL METABOLIC PATHWAYS.
CC -|- SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY.
CC -|- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC -----
CC EMBL: AF257590; AAC22891.1; -
CC EMBL: AF257591; AAC22893.1; -
CC EMBL: AF257592; AAC22895.1; -
CC EMBL: AF257593; AAC22897.1; -
CC EMBL: AF257594; AAC22899.1; -
CC EMBL: AF257595; AAC22901.1; -
CC EMBL: AF257596; AAC22903.1; -
CC EMBL: AF257597; AAC22905.1; -
CC EMBL: AF257598; AAC22907.1; -

DR EMBL: AF257599; AAC22909.1; -
DR EMBL: AF257600; AAC22911.1; -
DR EMBL: AF257601; AAC22913.1; -
DR EMBL: AF257602; AAC22915.1; -
DR EMBL: AF257603; AAC22917.1; -
DR EMBL: AF257604; AAC22919.1; -
DR EMBL: AF257605; AAC22921.1; -
DR EMBL: AF257606; AAC22923.1; -
DR EMBL: AF257607; AAC22925.1; -
DR EMBL: AF257608; AAC22927.1; -
DR EMBL: AJ271350; CAB72131.1; -
DR EMBL: AE003756; AAF56591.1; ALT_SEQ.
DR HSSP: Q26609; IBDG.
DR Flybase: FBgn0042711; Hex-1l.
DR InterPro: IPR001312; Hexokinase.
DR Pfam: PF00349; hexokinase.1.
DR Pfam: PF03727; hexokinase2.1.
DR PRINTS: PR00475; HEXOKINASE.
DR ProDom: PD001109; Hexokinase.1.
KW Transferase; Kinase; Glycolysis; ATP-binding;
KW Multigene family; Polymorphism.
FT BINDING 88
FT DOMAIN 139 165
FT VARIANT 33 33
FT VARIANT 243 243
FT VARIANT 243 243
FT Y->F (IN STRAINS DPF96E3_3.0,
FT DPF96E3_4.2, DPF96E3_23.1, DPF96E3_74.2,
FT VP97E3_41, SC96E3_12.3, HF197E3_8,
FT HF197E3_12, HF197E3_15, ZIM(S)E3_24,
FT ZIM(S)E3_35).
SQ SEQUENCE 465 AA; 52260 MW; 67B611920D5B6BDD CRC64;
Query Match 10.8%; Score 71; DB I; Length 465;
Best Local Similarity 30.8%; Pred. No. 7.6; 48; Indels 14; Gaps 5;
Matches 33; Conservative 12; Mismatches 48; Indels 14; Gaps 5;
QY I MYKLASCLLFTGFLNPLSLPLDSREISFOLSAPPEHARLTPPEELERASLLOILEPML 60
DB 14 YVKV---CKLFNPSIDDLKIKKMMREITMGSLRHHDSVTVCHL---SYVDLP--T 65
QY 61 GAERGDILRRADSSNTNFPNGNLRKF--QDFSGQDPNILLHLA 104
DB 66 GREGGQFLAEEMPTNC---RIMLVKFSRSDYITSSKCVIMPTVA 109
RESULT 10
ID MDH_STRCO STANDARD; PRT; 329 AA.
AC 09K3J3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Malate dehydrogenase (EC 1.1.1.37).
GN MDH OR SC04827 OR SC2A6.12.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RX MEDLINE=21996410; Pubmed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser I., Larke L., Murthy L., Oliver K., O'Neil S.,
RA Rabbittowitsch E., Rajandream M.A., Rutherford L., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";

```

DR HSP; P20393; 1A6Y.
DR TRANSFAC; T00850; -.
DR FLYBASE; FB9n0003862; trx.
DR InterPro: IPR003889; Fyricl_C.
DR InterPro: IPR003888; Fyricl_N.
DR InterPro: IPR003616; PostSET.
DR InterPro: IPR001214; SET.
DR InterPro: IPR001965; ZnF_PHD.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam; PF00628; PHD; 3.
DR Pfam; PF00856; SET; 1.
DR SMART; SM00542; FYRC; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00249; PHD; 4.
DR SMART; SM00508; PostSET; 1.
DR SMART; SM00184; RING; 3.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS00280; SET; 1.
DR PROSITE; PS01359; ZF_PHD_1; 4.
DR PROSITE; PS50016; ZF_PHD_2; 3.
DR Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
KW Nuclear protein; Developmental protein; Activator;
KW Alternative splicing.
KM
FT ZN_FING 1266 1347 PHD-TYPE 1.
FT ZN_FING 1348 1393 PHD-TYPE 2.
FT ZN_FING 1421 1482 PHD-TYPE 3.
FT ZN_FING 1734 1793 PHD-TYPE 4 (ATYPICAL).
FT ZN_FING 1794 1844 PHD-TYPE 5 (ATYPICAL).
FT DOMAIN 3599 3708 SET.
FT DOMAIN 512 516 POLY-SER.
FT DOMAIN 565 570 POLY-ASP.
FT DOMAIN 661 664 POLY-SER.
FT DOMAIN 905 910 POLY-SER.
FT DOMAIN 1576 1582 POLY-GLN.
FT DOMAIN 2298 3027 GLN-RICH.
FT DOMAIN 3032 3040 POLY-SER.
FT DOMAIN 3181 3184 POLY-GLN.
FT DOMAIN 3220 3225 POLY-GLU.
FT VARSPLIC 1 368 MISSING (IN SHORT ISOFORM).
FT CONFLICT 2025 P -> PWLTSPKFLGSLTHGGLMLLGLVVRUKQGG
FT CONFLICT 2341 R -> S (IN REF. 1).
FT CONFLICT 2392 G -> S (IN REF. 1).
SO SEQUENCE 3726 AA; 400575 MW; D2756E50763D1CF5 CRC64;

Query Match 12.1%; Score 79; DB 1; Length 3726;
Best Local Similarity 30.0%; Pred. No. 14;
Matches 24; Conservative 12; Mismatches 28; Indels 16; Gaps 3;

OY 29 ISFOLSAPEHDAARLTPEELERASLLQILPEMLGAERGDLIRKADSSTNIFNPRGNLRKFO 88
DB 857 ISFOLSAPEHDAARLTPEELERASLLQILPEMLGAERGDLIRKADSSTNIFNPRGNLRKFO 88
OY 89 DFGODPNILSHLARIWK 108
DB 903 TASSSSPSVASTSVK--WK 920

RESULT 8
ID 10D3_XENLA STANDARD; PRT; 271 AA.
AC P49899;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Type III Iodothyronine deiodinase (EC 3.8.1.4) (Type-III
DE 5'-deiodinase) (DIOIT1) (Type 3 DI) (5DIT1) (XL-15).
GN DIO3 OR TYD13 OR ITD13.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;

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RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE-94329597; PubMed-8052658;
RA St Germain D.L., Schwartzman R.A., Croteau W., Kanamori A., Wang Z.,
RA Brown D.D., Galton V.A.;
RT "A thyroid hormone-regulated gene in Xenopus laevis encodes a type
RT III Iodothyronine 5'-deiodinase."
RL Proc. Natl. Acad. Sci. U.S.A. 91:7767-7771(1994).
RN [2]
RP ERRATUM.
RX MEDLINE-95062251; PubMed-7972049;
RA St Germain D.L., Schwartzman R.A., Croteau W., Kanamori A., Wang Z.,
RA Brown D.D., Galton V.A.;
RL Proc. Natl. Acad. Sci. U.S.A. 91:11282-11282(1994).
CC -I- FUNCTION: RESPONSIBLE FOR THE DEIODINATION OF T4 (3,5,3',5'-
CC TETRAIODOTHYRONINE) INTO T3 (3,5,3'-TRIIODOTHYRONINE) AND OF T3
CC INTO T2 (3,3'-DIIODOTHYRONINE). MAY PLAY A PROTECTIVE ROLE IN
CC SELECTED TISSUES BY PREVENTING THEIR EXPOSURE TO INAPPROPRIATELY
CC TIMED OR EXCESSIVE LEVELS OF THYROID HORMONE.
CC -I- CATALYTIC ACTIVITY: L-thyroxine + H(2) = 3,5,3'-L-triiodo-L-
CC thyronine + Iodide + A + H(+).
CC -I- COFACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS
CC ENCODED BY THE OPAL CODON, UGA.
CC -I- SIMILARITY: BELONGS TO THE IODOOTHYRONINE DEIODINASE FAMILY.
CC -----
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CC -----
DR EMBL; L28111; AAA49971.2; ALT_SEQ.
DR InterPro: IPR000643; T4_deiodinase.
DR Pfam; PF00837; T4_deiodinase; 1.
DR PROSITE; PS01205; T4-DEIODINASE; 1.
KW Oxidoreductase; Hydrolase; Selenium; Selenocysteine.
FT SE_CYS 132 132
FT MUTAGEN 132 132 C->L. LOSS OF ENZYME ACTIVITY.
SO SEQUENCE 271 AA; 30252 MW; 64CFA26D9E9B51D CRC64;

Query Match 10.9%; Score 71.5; DB 1; Length 271;
Best Local Similarity 28.9%; Pred. No. 3.5;
Matches 33; Conservative 17; Mismatches 43; Indels 21; Gaps 5;

OY 3 KLASCLLFTGFLNPLSLPLD-----SREISFOLSAPHEHDAARLTPEELERAS 51
DB 15 GVAACCLLPRLFLTGLMGLMGLDFOCIRRVLLTARESS---TAHEHDPPLCVSDSNRC 71
OY 52 LQILPEMLGAERGDLIRKAD-----SSTNIFNPRG-NLRKQDPS-GODPNIL 98
DB 72 TVESLRAVWHGCKLDYFKSAHLGCSAPNTEVVMLEGRRLCKILDFSGGRPLV 125

RESULT 9
ID HKX1_DROME STANDARD; PRT; 465 AA.
AC Q9NFT9; Q9VBFL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hexokinase type 1 (EC 2.7.1.1).
GN HEX-T1 OR HEX OR CG5443.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Duvernell D.D., Eanes W.F.;

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DR MIM: 604097;
DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II: 1.
DR PROSITE: PS00984; UROSENSIN_II: 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PROPEP 21 110
FT PEPTIDE 114 124
FT DISULFID 118 123
FT CONFLICT 1 19
FT FT
FT CONFLICT 24 27
SQ SEQUENCE 124 AA: 14295 MW: C7A5FCIEFE00D312 CRC64:

Query Match
Best Local Similarity 100.0%; Score 655; DB 1; Length 124;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYKLASCLLFTIGFLNPLSLPLDSREISFQLSAPHEARLTPPELERASLQIIP EML 60
DB 1 MYKLASCLLFTIGFLNPLSLPLDSREISFQLSAPHEARLTPPELERASLQIIP EML 60
QY 61 GAERGDLIRKADSTNIFNRGNLRKFQDSGDDPNILLHLARIWKPKRKRETPDCFW 120
DB 61 GAERGDLIRKADSTNIFNRGNLRKFQDSGDDPNILLHLARIWKPKRKRETPDCFW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 2
UR2_MOUSE
ID UR2_MOUSE STANDARD; PRT; 123 AA.
AC 09QZ03;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urotensin II precursor (U-II) (UII).
GN UTS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Spinal cord;
RX MEDLINE=99416011; PubMed=10486557;
RA Cloutarn Y., Jegou S., Tostivint H., Vaudry H., Lohmann I.;
RT "Cloning, sequence analysis and tissue distribution of the mouse and
RT rat urotensin II precursors.";
RL FEBS Lett. 457:28-32(1999).
CC -1- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC. PREDOMINANTLY EXPRESSED IN
CC MOTONEURONS OF THE BRAINSTEM AND SPINAL CORD.
CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
CC -----
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CC -----
CC EMBL: AF172175; AAD55767.1;
CC MGD: MG1346329; UTS2.
CC InterPro: IPR001483; Urotensin_II.
CC Pfam: PF02083; Urotensin_II: 1.
CC PROSITE: PS00984; UROSENSIN_II: 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT CONFLICT 24 27
SQ SEQUENCE 123 AA: 13614 MW: E4FLA8E124AF1A CRC64:
```

```
FT PROPEP 21 104
FT PEPTIDE 110 123
FT DISULFID 117 122
SQ SEQUENCE 123 AA: 13625 MW: F96486195137F7E4 CRC64:

Query Match
Best Local Similarity 49.6%; Score 286.5; DB 1; Length 123;
Matches 62; Conservative 19; Mismatches 41; Indels 3; Gaps 2;

QY 1 MYKLASCLLFTIGFLNPLSLPLDSREISFQLSAPHEARLTPPELERASLQIIP EML 60
DB 1 MDRVPPCLLFTIGFLNPLSLPLDTPGERTQLPVEEDALRALEELERALLQITLRQTM 60
QY 61 GAERGDLIRKADSTNIFNRGNLRKFQDSGDDPNILLHLARIWKPKRKRETPDCFW 119
DB 61 GTEGESPEGAGSTETPTPRGSMRK--AFAGQNSNIVLSRLARTKQKHQGAPECF 118
QY 120 WKYCV 124
DB 119 WKYCI 123

RESULT 3
UR2_RAT
ID UR2_RAT STANDARD; PRT; 123 AA.
AC 09QZ04;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II precursor (U-II) (UII).
GN UTS2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Spinal cord;
RX MEDLINE=99416011; PubMed=10486557;
RA Cloutarn Y., Jegou S., Tostivint H., Vaudry H., Lohmann I.;
RT "Cloning, sequence analysis and tissue distribution of the mouse and
RT rat urotensin II precursors.";
RL FEBS Lett. 457:28-32(1999).
CC -1- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
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CC -----
CC EMBL: AF172174; AAD55766.1;
CC DR InterPro: IPR001483; Urotensin_II.
CC DR Pfam: PF02083; Urotensin_II: 1.
CC PROSITE: PS00984; UROSENSIN_II: 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PROPEP 21 104
FT PEPTIDE 110 123
FT DISULFID 117 122
SQ SEQUENCE 123 AA: 13614 MW: E4FLA8E124AF1A CRC64:

Query Match
Best Local Similarity 43.1%; Score 282.5; DB 1; Length 123;
Matches 62; Conservative 17; Mismatches 43; Indels 3; Gaps 2;

QY 1 MYKLASCLLFTIGFLNPLSLPLDSREISFQLSAPHEARLTPPELERASLQIIP EML 60
DB 1 MYKLASCLLFTIGFLNPLSLPLDSREISFQLSAPHEARLTPPELERASLQIIP EML 60
```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:26:37 ; Search time 7.03784 Seconds

(without alignments)
730.773 Million cell updates/sec

Title: US-09-831-907A-1

Perfect score: 655

Sequence: 1 MYKLASCCLEFGFLNPLLS.....RIMKPKKRETPDCFWKVCV 124

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	655	100.0	124	1	UR2_HUMAN
2	286.5	43.7	123	1	UR2_MOUSE
3	282.5	43.1	123	1	UR2_RAT
4	120.5	18.4	127	1	UR2_RANRI
5	90	13.7	125	1	UR2A_CYPCA
6	87.5	13.4	125	1	UR2B_CYPCA
7	79	12.1	3726	1	TRX_DROME
8	71.5	10.9	271	1	IOD3_XENLA
9	71	10.8	465	1	HXK1_DROME
10	70	10.7	329	1	MDH_STRCO
11	69	10.5	431	1	BMPT_HUMAN
12	69	10.5	525	1	NCAP_RINDL
13	68.5	10.5	373	1	DG1A_DEIRA
14	68.5	10.4	451	1	GNTF_ZYMO
15	68	10.4	319	1	COA_BACSU
16	68	10.4	508	1	COR1_MYCTU
17	66	10.1	412	1	EPH1_YEAST
18	66	10.1	686	1	Y1K5_YEAST
19	66	10.1	690	1	PERO_DROME
20	66	10.1	1780	1	YKZ6_CAEEL
21	65.5	10.0	455	1	NH55_CAEEL
22	65	9.9	591	1	TYPA_ECOLI
23	65	9.9	607	1	TYPA_ECO57
24	64.5	9.8	1121	1	DPOL_ADEG1
25	64.5	9.8	1201	1	MFD_MYXXA
26	64.5	9.8	1786	1	YCEL_ARATH
27	64	9.8	83	1	UR2_PLAFA
28	64	9.8	262	1	CHEK_CAMJE
29	64	9.8	376	1	EXD_DROME
30	64	9.8	408	1	GPT_CRILLO
31	64	9.8	465	1	AS3B_HUMAN
32	64	9.8	512	1	C4BL_DROME
33	64	9.8	956	1	SYL_AQUAE

ALIGNMENTS

RESULT 1	ID	UR2_HUMAN	STANDARD:	PRT:	124 AA.
AC	095399	Q9UKP7			
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Urotensin II precursor (U-II) (U11).				
GN	UTS2.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
ON	(1)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Spinal cord;				
RX	MEDLINE=99080095; PubMed=9861051;				
RA	Coulouarn Y., Lihmann I., Jegou S., Anouar Y., Tostivint H.,				
RA	Beauvillain J.C., Conlon J.M., Bern H.A., Vaudry H.;				
RT	"Cloning of the cDNA encoding the urotensin II precursor in frog and				
RT	human reveals intense expression of the urotensin II gene in				
RT	motoneurons of the spinal cord";				
RL	Proc. Natl. Acad. Sci. U.S.A. 95:15803-15808(1998).				
RN	(2)				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=99427933; PubMed=10499587;				
RA	Ames R.S., Sarau H.M., Chambers J.K., Willette R.N., Aiyar N.V.,				
RA	Romanic A.M., Loudon C.S., Foley J.J., Sauermelch C.F., Coatsney R.W.,				
RA	Ho Z., Disa J., Holmes S.D., Stadel J.M., Martin J.D., Liu W.-S.,				
RA	Shover G.I., Wilson S., McNulty D.E., Ellis C.E., Elshourbagy N.A.,				
RA	Shabon U., Trill J.J., Hay D.W.P., Ohlstein E.H., Bergsma D.J.,				
RA	Douglas S.A.;				
RT	"Human urotensin-II is a potent vasoconstrictor and agonist for the				
RT	orphan receptor GPR14";				
RL	Nature 401:282-286(1999).				
RN	(3)				
RP	SEQUENCE FROM N.A.				
RA	Pearce A.;				
CC	Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.				
CC	- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR.				
CC	- SUBCELLULAR LOCATION: Secreted.				
CC	- TISSUE SPECIFICITY: BRAIN-SPECIFIC.				
CC	- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.				
CC	-----				
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CC	or send an email to license@sib-sib.ch).				
CC	-----				
CC	EMBL: AF104118; AAD13070.1; -				
CC	EMBL: AF140630; AAD55577.1; -				
CC	EMBL: Z38884; CAB63148.1; -				
CC	Genew: HGNC:12636; UTS2.				

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0y 23 LIDSEIFFO---LSAPHEDARLRLPELEASL---LQILPEMLGAEGRDILRKADST 75
      | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 54 LVSSEILDQONLIS-----MLPEERSRAGLFGVQMPLEPVGNNKMFLLDA--- 102
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
0y 76 NIFNPGMLRKRFQDPGSDPNILLSHLARIWKDYKKRETPDC 119
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 103 ---YNAARRANQEGDISIDFETFTLLSTYL---ETFEYNATTDLF 140
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

```

RESULT 11
H86576
ABC transporter ATPase [imported] - Chlamydomophila pneumoniae (strain J138)
C.Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C.Accession: H86576
R.Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A.Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A.Reference number: A86451; MUID:20330349; PMID:10871362
A.Accession: H86576
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-256 <STO>
A.Cross-references: GB:BA000008; NID:98979065; PIDN:BA98898.1; GSPDB:GN00142
A.Experimental source: strain J138
C.Genetics:
A:Gene: abcx
A:Superfamily: unassigned ATP-binding cassette proteins: ATP-binding cassette

```

Query Match	11.1%	Score 73;	DB 2;	Length 256;
Best Local Similarity	31.7%;	Pred. No. 6.5;		
Matches	33;	Conservative	11;	Mismatches 36;
			Indels 24;	Gaps 5;
QY	23	LIDREISFQ----LSAPHEDARLTPEELERASL---	LQILPEMIGAERGLIKRADSSST	75
		: :	: :	
Db	54	LVSSGETALDQONLIS-----MLPERSRAGLTVGFQMPPEITPGVNNKFLRDA----		102
		: :	: :	
QY	76	NIFNPGNLRFQDFSGODPNILLSHLARLIMPKKKRETPDCCF		119
		: :	: :	
Db	103	-YIARRRANQEGDISIDDEFNTLLSTVL-----ETYEYVATTDLDF		140

```

RESULT 12
T19241
hypothetical protein C13G3.3a - Caenorhabditis elegans
C:Species:Caenorhabditis elegans
C:Date:15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19241
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19096
A:Accession: T19241
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-557 <MIL>
A:Cross-references: EMBL:Z74027; PIDN:CAA98422.1; GSPDB:GN00023; CESP:C13G3.3a
A:Experimental source: clone C13G3
C:Genetics:
A:Gene: CESP:C13G3.3a
A:Map position: 5
A:Introns: 21/1; 52/1; 156/3; 510/3

```

Query Match	11.1%	Score 72.5	DB 2	Length 557	
Best Local Similarity	26.4%	Pred. No. 18			
Matches	23	Conservative	17	Mismatches	14
				Indels	33
				Gaps	5
QY	3	KLASCCLLFIIFLPLPLSLPLDLSREISFQSLAPHEDARLPRELETERASLLQILPMLGA	62		
Db	65	KLRCQCVAF-DFANDALS-----KEYKRALNELVDPVHSGA	103		
		DLKF-----			
QY	63	ERGDILKRADS-----STNIFNP	80		

```
Db 104 PKGSL--SDAVYPEAIGMFSTNLF RP 127
```

RESULT 13
T19242
hypothetical protein C13G3.3b - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19242

A:Submitted to the EMBL Data Library, June 1996
A:Reference number: Z19096
A:Accession: T19242
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-561 <MIL>
A:Cross-references: EMBL:Z74027; PIDN:CAA98423.1; GSPDB:GN00023; CESP:CL363.3b
A:Experimental source: clone CL363
C:Genetics:
A:Gene: CESP:CL363.3b
A:Map position: 5
A:Introns: 21/1; 56/1; 160/3; 514/3

Query Match	11.1%	Score 72.5	DB 2	Length 561
Best Local Similarity	26.4%	Pred NO. 18		
Matches 23	Conservative 17	Mismatches 14	Indels 33	Gaps 5

```

QY 3 KLASCLFGEFNPLPLSLPDSNEISFQSLSAHNEARLTPETLPRASLQIPLPMGLA 62
   || || || || || || || || || || || || || || || || || || || || ||
Db 69 KLNQCCVE-DRANDALS-----DLNF-----RKVKKAALNELVAVSQA 10
                                     -
QY 63 ERGDIIRKADS-----STNIFNP 80
   : : : : ||| : |
Db 108 PKGSL--SDAVYPAEIGNFSTNIFRP 131

```

RESULT 14
T20890
hypothetical protein F40G12.11 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T20890; T22062
R:Berks, M.
submitted to the EMBL Data Library, July 1996
#:Reference number: Z19340

A:Cross-references: EMBL:Z77658; PIDN:CA01162.1; GSPDB:GNO0023; CESP:F40G12.11
A:Experimental source: clone F14D7
R:McMurray, A.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19507
A:Accession: T22062
A:Status: preliminary; translated from GR/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-381 <WT2>
A:Cross-references: EMBL:Z77661; PIDN:CA01191.1; GSPDB:GNO0023; CESP:F40G12.11
A:Experimental source: clone F40G12
C:Genetics:
A:Gene: CESP:F40G12.11
A:Map position: 5
A:Introns: 100/3; 261/2

```

Query Match Similarity 10 8% Score 71: DB 2: Length 381:
Best Local Similarity 21 8% Pred. No. 17:
Matches 24: Conservative 17: Mismatches 35: Indels 34: Gaps 3:

QY 1 MYKASCCLLTGTGPNPLSLPDLDSREISFOLSAPHEDARTLPPELERASLIQIIPENL 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 126 LYALSERKLTIRAGVINOPL-----PTERRRSKSTPTFLENMNAALSTSL 169

```

A:Cross-references: GB:AE00113; GB:AE000782; NID:g2689436; PIDN:AA891305.1; PID:g265073
 C:Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF2358

Query Match 11.8%; Score 77; DB 2; Length 392;
 Best Local Similarity 24.1%; Pred. No. 4.1;
 Matches 26; Conservative 25; Mismatches 31; Indels 26; Gaps 6;

OY 12 IGFNLPLSLPLDSRLSFLSAPHSAPHDARLTPPELRASLIQLPEMLGAEERDIIRKA 71
 DB 274 IPEKLELLKTRKKKGRKME---HESC---GQQLKRA-----MIPLEKELIKDK 318
 OY 72 DSSNIFNPRGNLKKFOD-----FSGODPNILLSHLARI-WKPYK 111
 DB 319 NKRFVL---GDLRKFADQMAKDITKMTSNKNVILTHNVSSVDQHYK 363

RESULT 7
 G72575
 hypothetical protein APE1887 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: G72575
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K DNA Res. 6; 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
 A:Reference number: A72450; MUID:99310393; PMID:10382966
 A:Accession: G72575
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-433 <RAW>
 A:Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80892.1; PID:d1044678; PID:g510
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1887

Query Match 11.7%; Score 76.5; DB 2; Length 433;
 Best Local Similarity 29.5%; Pred. No. 5.2;
 Matches 33; Conservative 13; Mismatches 29; Indels 37; Gaps 7;

OY 23 LLDSEISFQLSAPHD-ARL-----TPRELRASLIQLPEMLGAE---RGDILRKA 71
 DB 171 LVSSR-----AWHEDLARLGVELVEVDPIEFARVVAESVPSLGEVLRGCEVLDLA 223
 OY 72 DSSNIFNPRGNLKKFODFSGODPNILLSHLARIWKPY-KKREPPDFWKY 122
 DB 224 DG-----EPKNSLRVYR-----AIKRMKSRGUDAVSPACWRFY 257

RESULT 8
 E86170
 hypothetical protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E86170
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408; 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Malt, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E86170
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-534 <STO>
 A:Cross-references: GB:AE005172; NID:g4204293; PIDN:AA010674.1; GSPDB:GNO0141
 C:Genetics:
 A:Map position: 1

Query Match 11.4%; Score 74.5; DB 2; Length 534;
 Best Local Similarity 26.0%; Pred. No. 11;
 Matches 27; Conservative 21; Mismatches 33; Indels 23; Gaps 4;

OY 23 LLDSEISF---QLSAPHDARLTPPELRASLIQLPEMLGAEERDI-----LRKADS 73
 DB 405 VITSNEMOFFEEDL---HRMECTQEAIVLSFDILCOIDIGEEKENCITLQDLKSGKL 461
 OY 74 STNIFNPRGNLKKFODFSGODPNILLSHLARIWKPYKRETPD 117
 DB 462 SANVFNLPLNKKFMARETRDPFLI-----RQERDPN 494

RESULT 9
 G90092
 hypothetical protein U5 snRNP [imported] - Guillardia theta nucleomorph
 C:Species: nucleomorph Guillardia theta
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: G90092
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Nature 410; 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: G90092
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-827 <DOU>
 A:Cross-references: GB:AF165818; NID:g13794496; PIDN:AAK39871.1; GSPDB:GNO0150
 C:Genetics:
 A:Gene: U5 snRNP
 A:Map position: 1
 A:Genome: nucleomorph
 C:Keywords: nucleomorph

Query Match 11.4%; Score 74.5; DB 2; Length 827;
 Best Local Similarity 28.0%; Pred. No. 18;
 Matches 26; Conservative 16; Mismatches 30; Indels 21; Gaps 5;

OY 39 DARLTPPELRASLIQLPEMLGAEERDILRK---ADSSNIFN-----RCNL 84
 DB 192 ELKMPDDEVK-RILQIDELNYLALHKVINKSVSKNNINFFNLNDNVCRSALSGWI 250
 OY 85 RKFDGSC---QDPNILLSH--LLARIWKPYK 111
 DB 251 FNLNFGSLYMSQPSICLSQKDSERIMNDKK 283

RESULT 10
 A72048
 ABC transporter ATPase - Chlamydomonas reinhardtii (strain CW1029)
 C:Species: Chlamydomonas reinhardtii
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
 C:Accession: A72048
 R:Kaltman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, Nature Genet. 21; 385-389, 1999
 A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: A72048
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-256 <RAW>
 A:Cross-references: GB:AE001651; GB:AE001363; NID:g4376985; PIDN:AA018830.1; PID:g437
 A:Experimental source: strain CW1029
 C:Genetics:
 A:Gene: abcX
 C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
 E:17-227/Domain: ATP-binding cassette homolog <ABC>

Query Match 11.1%; Score 73; DB 2; Length 256;
 Best Local Similarity 31.7%; Pred. No. 6.5;
 Matches 33; Conservative 11; Mismatches 36; Indels 24; Gaps 5;

2

A;Residues: 1-392 <KLE>

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: March 10, 2003, 17:36:23 ; Search time 13.4054 Seconds
(without alignments)
889.243 Million cell updates/sec

Title: US-09-831-907A-1

Perfect score: 655
Sequence: 1 MYKLASCCLLFIFGLNPLLS.....RIWKPKKRETPDCFWKVCV 124

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	13.7	125	2	I50498	urotensin II-alpha
2	87.5	13.4	125	2	I50499	urotensin II-gamma
3	80	12.2	140	2	T44815	hypothetical prote
4	79.5	12.1	469	2	T48314	hypothetical prote
5	79	12.1	3759	2	A35085	trilhorax protein
6	77	11.8	392	2	F69544	conserved hypotet
7	76.5	11.7	433	2	G72575	hypothetical prote
8	74.5	11.4	534	2	E86170	hypothetical prote
9	74.5	11.4	827	2	G90092	hypothetical prote
10	73	11.1	256	2	A72048	ABC transporter AT
11	73	11.1	256	2	H86576	hypothetical prote
12	72.5	11.1	557	2	T19241	hypothetical prote
13	72.5	11.1	561	2	T19242	hypothetical prote
14	71	10.8	381	2	T20890	hypothetical prote
15	70.5	10.8	321	2	T01521	synthaxin homolog T
16	70.5	10.8	411	2	B84504	probable retroelem
17	70.5	10.8	1131	2	AD2166	two-component sens
18	70	10.7	815	2	F86311	fla6.2 protein -
19	69.5	10.6	334	2	C70813	hypothetical prote
20	69.5	10.6	336	2	T08338	hypothetical prote
21	69.5	10.6	1791	2	T02345	hypothetical prote
22	69	10.5	431	1	BMH07	bone morphogenetic
23	69	10.5	694	2	T01134	probable protein k
24	69	10.5	1667	2	T15863	hypothetical prote
25	68.5	10.5	373	2	F75449	dGTP triphosphohyd
26	68.5	10.5	433	2	S52837	slit protein - fls
27	68.5	10.5	455	2	T47921	hypothetical prote
28	68.5	10.5	561	2	T36084	hypothetical prote
29	68.5	10.5	1016	2	T05066	hypothetical prote

30	68	10.4	293	2	C69965	Pantothenate kinas
31	68	10.4	508	2	E70764	probable cobi prot
32	68	10.4	754	2	A85043	probable LRR recep
33	67.5	10.3	312	2	T41157	probable 60s acid
34	67	10.2	326	2	E86647	prenyl transferase
35	67	10.2	431	2	T38260	hypothetical prote
36	67	10.2	834	2	T39891	probable integral
37	67	10.2	859	2	T46372	hypothetical prote
38	67	10.2	1953	2	T40642	probable helicase
39	66.5	10.2	734	2	T02196	hypothetical prote
40	66	10.1	366	2	E84265	hypothetical prote
41	66	10.1	412	2	S37906	translation elonga
42	66	10.1	475	2	H84773	hypothetical prote
43	66	10.1	686	2	S48467	hypothetical prote
44	66	10.1	690	2	S28222	peroxidase (EC 1.1
45	66	10.1	789	2	S44759	C14B9.5 protein -

ALIGNMENTS

RESULT 1

150498

urotensin II-alpha precursor - common carp

C:Species: Cyprinus carpio (common carp)

C:Date: 13-Sep-1996 #sequence-revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: 150498

R:Onsako, S.; Ishida, I.; Ichikawa, T.; Deguchi, T.

J. Neurosci. 6, 2730-2735, 1986

A:Title: Cloning and sequence analysis of cDNAs encoding precursors of urotensin II-a

A:Reference number: 150498; PMID:86307061; PMID:2427672

A:Accession: 150498

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-125 <OHS>

A:Cross-references: GB:M14084; NID:g213066; PIDN:AAA49215.1; PID:g213067

C:Superfamily: urotensin II

Query Match 13.7%; Score 90; DB 2; Length 125;
Best Local Similarity 26.8%; Pred. No. 0.049;

Matches 38; Conservative 16; Mismatches 44; Indels 44; Gaps 7;

QY 8 CLPFIQFLNPLLSL-----PLDSREISFQLSAP---HEDARLPPELEASLIQLPE 58

Db 3 CNLLISFVLLSCTHLVAHPVTDTADMT--SGPDSVEEGVSPDFAVSLNDLLQR 60

QY 59 MGAERGDI LRKADSTNIFNPRGNLRKFQDFSGDPNILLSHLARIWKPY----- 110

Db 61 AAVEYSPL-----SRENKYP-----GQIKKALRELL--LEKRYRLIPSGL 103

QY 111 -----KKRETPDCFWKVCV 124

Db 104 WGSRRQFRKRGGADCFWKVCV 125

RESULT 2

150499

urotensin II-gamma precursor - common carp

C:Species: Cyprinus carpio (common carp)

C:Date: 13-Sep-1996 #sequence-revision 13-Sep-1996 #text_change 16-Jul-1999

C:Accession: 150499

R:Onsako, S.; Ishida, I.; Ichikawa, T.; Deguchi, T.

J. Neurosci. 6, 2730-2735, 1986

A:Title: Cloning and sequence analysis of cDNAs encoding precursors of urotensin II-a

A:Reference number: 150498; PMID:86307061; PMID:2427672

A:Accession: 150499

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-125 <OHS>

A:Cross-references: GB:M14088; NID:g213068; PIDN:AAA49216.1; PID:g213069

C:Superfamily: urotensin II

Query Match 13.4%; Score 87.5; DB 2; Length 125;

Tue Mar 11 10:10:10 2003

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Best Local Similarity	99.2%	Pred. NO. 3.2e-66:		
Matches 123, Conservative	0:	Mismatches 1:	Indels 0:	Gaps 0

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Db      1 MYKLASCCLETFGLNPLNLSLPILDSREISFQLSAPHEBARLNPPEELERSLLQIPEML 60
QY      61 GAERGDILRKADSSNTFNPNRGNLRKFODFSGODPNLLSHLARLWPKYKRETFDCEW 120
Db      61 GAERGDILRKADSSNTFNPNRGNLRKFODESGODPNLLSHLARLWPKYKRETFDCEW 120
QY      121 KYCV 124
Db      121 KYCV 124

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Search completed: March 10, 2003, 17:48:53
Job time : 10.7189 secs

APPLICANT: Zhang, Zemu
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C2
CURRENT APPLICATION NUMBER: US/09/997,666
CURRENT FILING DATE: 2001-11-15
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
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PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090557
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PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3.2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MYKLSCCLFGLFGLNPLLSPLLDREISFQLSAPHEDARLTPEELERASLLQTLPEML 60
Db 1 MYKLSCCLFGLFGLNPLLSPLLDREISFQLSAPHEDARLTPEELERASLLQTLPEML 60
Qy 61 GAERGDILRKADSTNINFPNGNLKRFQDFSGQDPNILLSHLLARIWPKYKRETPDDCFW 120
Db 61 GAERGDILRKADSTNINFPNGNLKRFQDFSGQDPNILLSHLLARIWPKYKRETPDDCFW 120
Qy 121 KYCV 124
Db 121 KYCV 124

RESULT 15
US-09-997-666-266
Sequence 266, Application US/09997666
Publication No. US20030027163A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerilsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.

PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3, 2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYKASCCLETFGLPLSLPLDSREISFQLSAPHEADRLTPEELERASLLQILPEML 60
DB 1 MYKASCCLETFGLPLSLPLDSREISFQLSAPHEADRLTPEELERASLLQILPEML 60
QY 61 GAERGDILKKAASSTNIENPRGNLRFQDFSGODPNIILSHLARIWKYKKRETPDCW 120
DB 61 GAERGDILKKAASSTNIENPRGNLRFQDFSGODPNIILSHLARIWKYKKRETPDCW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 14
US-09-997-428-266
Sequence 266, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaud, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavyn, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/997,428
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC18
PRIOR APPLICATION NUMBER: US/09/990,562
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
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PRIOR FILING DATE: 1998-02-25
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PRIOR APPLICATION NUMBER: 60/084600
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PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861

PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25

PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695

PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3,2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYKLASCCLLFGLFNPILSLPLDLSREISFQLSAPHEDARTPELEBRASLQILPEML 60
DB 1 MYKLASCCLLFGLFNPILSLPLDLSREISFQLSAPHEDARTPELEBRASLQILPEML 60
QY 61 GAERGDILRKADSSNIFNPRGNLRKPODFSGOPNILLSLLARIMKPYKRETPDCFW 120
DB 61 GAERGDILRKADSSNIFNPRGNLRKPODFSGOPNILLSLLARIMKPYKRETPDCFW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 13
US-09-990-562-266
Sequence 266, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferreira, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlson, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3 2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYKLASCLLFTGFLNPLSLPLDSREISFQLSAPHEDARLPEELERASLLQILPEML 60
DB 1 MYKLASCLLFTGFLNPLSLPLDSREISFQLSAPHEDARLPEELERASLLQILPEML 60
QY 61 GAERGDLIRKADSTNIFNPRGNLRKFQDSGQDPNILLSHLARIKPKYKKRTPPCFW 120
DB 61 GAERGDLIRKADSTNIFNPRGNLRKFQDSGQDPNILLSHLARIKPKYKKRTPPCFW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 12
US-09-990-438-266
Sequence 266, Application US/09990438
Publication No. US2003002754A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin J.
APPLICANT: Kiljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730PIC3
CURRENT APPLICATION NUMBER: US/09/990,438
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2% Score 650; DB 9; Length 124;
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QY 61 GAERGDILKRKADSTNIENPRGNLRRFQDFSGODPNILLSHLLARIMKRYKRRPPDCFW 120
DB 61 GAERGDILKRKADSTNIENPRGNLRRFQDFSGODPNILLSHLLARIMKRYKRRPPDCFW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 11
US-09-993-667-266
Sequence 266, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pabni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C4

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; PRIOR FILING DATE: 1998-07-09

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Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 121 KYCV 124
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
; CURRENT APPLICATION NUMBER: US/09/997, 653

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70	PRIOR FILING DATE: 1998-06-25
71	PRIOR APPLICATION NUMBER: 60/090701
72	PRIOR FILING DATE: 1998-06-25
73	PRIOR APPLICATION NUMBER: 60/090702
74	PRIOR FILING DATE: 1998-06-25
75	PRIOR APPLICATION NUMBER: 60/090703
76	PRIOR FILING DATE: 1998-06-25
77	PRIOR APPLICATION NUMBER: 60/090704
78	PRIOR FILING DATE: 1998-06-25
79	PRIOR APPLICATION NUMBER: 60/090705
80	PRIOR FILING DATE: 1998-06-25
81	PRIOR APPLICATION NUMBER: 60/090706
82	PRIOR FILING DATE: 1998-06-25
83	PRIOR APPLICATION NUMBER: 60/090707
84	PRIOR FILING DATE: 1998-06-25
85	PRIOR APPLICATION NUMBER: 60/090708
86	PRIOR FILING DATE: 1998-06-25
87	PRIOR APPLICATION NUMBER: 60/090709
88	PRIOR FILING DATE: 1998-06-25
89	PRIOR APPLICATION NUMBER: 60/090710
90	PRIOR FILING DATE: 1998-06-25
91	PRIOR APPLICATION NUMBER: 60/090711
92	PRIOR FILING DATE: 1998-06-25
93	PRIOR APPLICATION NUMBER: 60/090712
94	PRIOR FILING DATE: 1998-06-25
95	PRIOR APPLICATION NUMBER: 60/090713
96	PRIOR FILING DATE: 1998-06-25
97	PRIOR APPLICATION NUMBER: 60/090714
98	PRIOR FILING DATE: 1998-06-25
99	PRIOR APPLICATION NUMBER: 60/090715
100	PRIOR FILING DATE: 1998-06-25

1 PRIOR FILING DATE: 1998-06-26
2 PRIOR APPLICATION NUMBER: 60/090863
3 PRIOR FILING DATE: 1998-06-26
4 PRIOR APPLICATION NUMBER: 60/091360
5 PRIOR FILING DATE: 1998-07-01
6 PRIOR APPLICATION NUMBER: 60/091478
7 PRIOR FILING DATE: 1998-07-02
8 PRIOR APPLICATION NUMBER: 60/091544
9 PRIOR FILING DATE: 1998-07-01
10 PRIOR APPLICATION NUMBER: 60/091519
11 PRIOR FILING DATE: 1998-07-02
12 PRIOR APPLICATION NUMBER: 60/091626
13 PRIOR FILING DATE: 1998-07-02
14 PRIOR APPLICATION NUMBER: 60/091633
15 PRIOR FILING DATE: 1998-07-02
16 PRIOR APPLICATION NUMBER: 60/091978
17 PRIOR FILING DATE: 1998-07-07
18 PRIOR APPLICATION NUMBER: 60/091982
19 PRIOR FILING DATE: 1998-07-07
20 PRIOR APPLICATION NUMBER: 60/092182
21 PRIOR FILING DATE: 1998-07-09

Query Match	99.28;	Score 650;	DB 9;	Length 124;
Best Local, Similarity	99.28;	Pred. No. 3.2e-66;		
Matches 123; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

[illegible]

Oy	121	KYCV	124
		1111	
Db	121	KYCV	124

RESULT 9
 US-09-989-734-266
 : Sequence 266, Application US/09989734
 : Publication No. US20030003531A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi J.
 : APPLICANT: Baker, Kevin P.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnoyers, Luc
 : APPLICANT: Eaton, Dan L.
 : APPLICANT: Ferrara, Napoleone
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Kljavin, Ivar J.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James
 : APPLICANT: Paoni, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Watanabe, Colin K.
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William I.
 : APPLICANT: Zhang, Zemin
 : TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
 : TITLE OF INVENTION: Acids Encoding the Same
 : FILE REFERENCE: P2730P1C64
 : CURRENT APPLICATION NUMBER: US/09/989, 734
 : CURRENT FILING DATE: 2001-11-19

PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/0899512
PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/0899514
PRIOR FILING DATE: 1998-06-16	PRIOR APPLICATION NUMBER: 60/0895352
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/0895380
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/0895388
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/0895599
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/0896000
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/0896533
PRIOR FILING DATE: 1998-06-17	PRIOR APPLICATION NUMBER: 60/0898001
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/0898907
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/0899080
PRIOR FILING DATE: 1998-06-18	PRIOR APPLICATION NUMBER: 60/0899474
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/0899498
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/0899522
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/0899525
PRIOR FILING DATE: 1998-06-19	PRIOR APPLICATION NUMBER: 60/0902466
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/0902522
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/0902544
PRIOR FILING DATE: 1998-06-22	PRIOR APPLICATION NUMBER: 60/0903499
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0904313
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0904355
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0904444
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0904455
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0904722
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0905353
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0905404
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0905575
PRIOR FILING DATE: 1998-06-24	PRIOR APPLICATION NUMBER: 60/0906178
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/0906625
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/0906949
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/0906955
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/0906969
PRIOR FILING DATE: 1998-06-25	PRIOR APPLICATION NUMBER: 60/0908674
PRIOR FILING DATE: 1998-06-26	PRIOR APPLICATION NUMBER: 60/0908676

PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/090542
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PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863

PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3.2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYKLASCLLFTGFLNPLSLPLDLSREISFOLSAPHEDARLTPEELERASLLQILPEML 60
|||||

DB 1 MYKLASCLLFTGFLNPLSLPLDLSREISFOLSAPHEDARLTPEELERASLLQILPEML 60

QY 61 GAERDILRKADSTNIENPRGNLRRKQDFSGODPNILLSHLARIWPKYKRRTPDCFW 120
|||||

DB 61 GAERDILRKADSTNIENPRGNLRRKQDFSGODPNILLSHLARIWPKYKRRTPDCFW 120

QY 121 KYCV 124
||||

DB 121 KYCV 124

RESULT 7

US-09-991-181-266

Sequence 266, Application US/09991181

Publication No. US20020197615A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botsstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerder, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2730PIC53

CURRENT APPLICATION NUMBER: US/09/991,181

CURRENT FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE:	1997-10-17
PRIOR APPLICATION NUMBER:	60/065186
PRIOR FILING DATE:	1997-11-12
PRIOR APPLICATION NUMBER:	60/065311
PRIOR FILING DATE:	1997-11-13
PRIOR APPLICATION NUMBER:	60/066770
PRIOR FILING DATE:	1997-11-24
PRIOR APPLICATION NUMBER:	60/075945
PRIOR FILING DATE:	1998-02-25
PRIOR APPLICATION NUMBER:	60/078910
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
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PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/087106
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360

PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3.2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MYKLASCCLEFICFLNPLSLPLDLSREISFOLSAPHEPARLTPPELEERASLLOILPEML 60
Db 1 MYKLASCCLEFICFLNPLSLPLDLSREISFOLSAPHEPARLTPPELEERASLLOILPEML 60

Qy 61 GAERCDILRKADSTNIFNPGNLKRFODFSGODPNILSLHLARITMKPKKRETPDCFW 120
Db 61 GAERCDILRKADSTNIFNPGNLKRFODFSGODPNILSLHLARITMKPKKRETPDCFW 120

Qy 121 KYCV 124
Db 121 KYCV 124

RESULT 5
US-09-989-730-266
Sequence 266, Application US/09989730
Publication No. US20020197674A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC69
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2% Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3, 2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MYKLASCCLLFTGFLNPLSLPLDLSREISFOLSAPEHDARLTPEELERASLLQILPEML 60
|||||
DB 1 MYKLASCCLLFTGFLNPLSLPLDLSREISFOLSAPEHDARLTPEELERASLLQILPEML 60
|||||

OY 61 GAERGDILRKADSTNIFNPRGNLRKRFODESGODPNILLSHLLARIIMKPKKRETPDCFW 120
|||||
DB 61 GAERGDILRKADSTNIFNPRGNLRKRFODESGODPNILLSHLLARIIMKPKKRETPDCFW 120
|||||

OY 121 KYCV 124
|||||
DB 121 KYCV 124

RESULT 4
US-09-990-444-266
Sequence 266, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/990,444
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
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PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
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29	PRIOR FILING DATE: 1998-06-23
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38	PRIOR APPLICATION NUMBER: 60/090535
39	PRIOR FILING DATE: 1998-06-24
40	PRIOR APPLICATION NUMBER: 60/090540
41	PRIOR FILING DATE: 1998-06-24
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52	PRIOR APPLICATION NUMBER: 60/090694
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65	PRIOR FILING DATE: 1998-07-01

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1 PRIOR FILING DATE: 1998-07-02
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11 PRIOR FILING DATE: 1998-07-07
12 PRIOR APPLICATION NUMBER: 60/091982
13 PRIOR FILING DATE: 1998-07-07
14 PRIOR APPLICATION NUMBER: 60/092182
15 PRIOR FILING DATE: 1998-07-09

Query Match	99.28;	Score 650;	DB 9;	Length 124;
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QY	1	MYKLASCCLLFTGFLNPLLSPLPLDLSREISFQLSAPHEDARLTPEEELERASLQIPEML	60
Db	1	MYKLASCCLLFTGFLNPLLSPLPLDLSREISFQLSAPHEDARLTPEEELERASLQIPEML	60
QY	61	GAERGDI LRKADSSSTNIFNPRGNLRKTFQDSFGQDPNILLSHLARIMKPYKRRTPDCFW	120
Db	61	GAERGDI LRKADSSSTNIFNPRGNLRKTFQDSFGQDPNILLSHLARIMKPYKRRTPDCFW	120
QY	121	KYCV 124	
Db	121	KYCV 124	

RESULT 3
HS-09-98

US-09-989-735-266

sequence 266, Application US/09989735

Publication No. US20020193299A1

; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Borstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PJC61
 CURRENT APPLICATION NUMBER: US/09/989,735
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
 PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 99.2%; Score 650; DB 9; Length 124;
Best Local Similarity 99.2%; Pred. No. 3, 2e-66;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MYKLASCLLFTGLNPLSLPLDLSREISFQLSAPHEARLTPPELEASLLQILPEML 60
QY 61 GAEKGDLRKADSTNIFNPRGNLRFQDFSGDDPNLLSHLARIMKPKKRETPDCFW 120
DB 61 GAEKGDLRKADSTNIFNPRGNLRFQDFSGDDPNLLSHLARIMKPKKRETPDCFW 120

QY 121 KYCV 124
DB 121 KYCV 124

RESULT 2
US-09-989-293a-266
Sequence 266, Application US/09989293A

Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guiney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C66
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[illegible]

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:38:48 ; Search time 9.71892 Seconds
(without alignments)
538.033 Million cell updates/sec

Title: US-09-831-907A-1

Perfect score: 655
Sequence: 1 MYKLASCLFIFGLNPLS.....RIMKPKKRETPDCFWKVCV 124

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	650	99.2	124	9	US-09-989-293A-266
3	650	99.2	124	9	US-09-989-735-266
4	650	99.2	124	9	US-09-990-444-266
5	650	99.2	124	9	US-09-989-730-266
6	650	99.2	124	9	US-09-990-436-266
7	650	99.2	124	9	US-09-991-181-266
8	650	99.2	124	9	US-09-993-687-266
9	650	99.2	124	9	US-09-989-734-266
10	650	99.2	124	9	US-09-997-653-266
11	650	99.2	124	9	US-09-993-667-266
12	650	99.2	124	9	US-09-990-438-266
13	650	99.2	124	9	US-09-990-562-266
14	650	99.2	124	9	US-09-997-428-266
15	650	99.2	124	9	US-09-997-666-266
16	650	99.2	124	9	US-09-990-711-266
17	650	99.2	124	9	US-09-989-726-266
18	650	99.2	124	10	US-09-989-722-266
19	650	99.2	124	10	US-09-989-723-266

20	650	99.2	124	10	US-09-989-279-266	Sequence 266, App
21	650	99.2	124	10	US-09-989-727-266	Sequence 266, App
22	650	99.2	124	10	US-09-989-721-266	Sequence 266, App
23	650	99.2	124	10	US-09-989-732-266	Sequence 266, App
24	650	99.2	124	10	US-09-991-073-266	Sequence 266, App
25	650	99.2	124	10	US-09-990-442-266	Sequence 266, App
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28	650	99.2	124	10	US-09-990-456-266	Sequence 266, App
29	650	99.2	124	10	US-09-989-721-266	Sequence 266, App
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31	71	10.8	465	10	US-09-815-242-10512	Sequence 10512, A
32	69	10.5	431	8	US-08-822-186-2	Sequence 2, Appl1
33	69	10.5	431	8	US-08-937-755-2	Sequence 2, Appl1
34	69	10.5	431	9	US-09-982-543A-10	Sequence 10, Appl1
35	69	10.5	431	9	US-10-062-370-5	Sequence 5, Appl1
36	69	10.5	431	9	US-09-039-107-2	Sequence 2, Appl1
37	69	10.5	431	10	US-09-045-331-2	Sequence 2, Appl1
38	69	10.5	431	10	US-09-828-607-2	Sequence 2, Appl1
39	69	10.5	432	10	US-09-361-741-3	Sequence 3, Appl1
40	66	10.1	437	9	US-10-156-239-49	Sequence 49, Appl1
41	66	10.1	437	10	US-09-808-568-2	Sequence 2, Appl1
42	66	10.1	783	10	US-09-888-615-67	Sequence 67, Appl1
43	66	10.1	814	9	US-10-156-239-52	Sequence 52, Appl1
44	66	10.1	814	10	US-09-808-568-5	Sequence 5, Appl1
45	65.5	10.0	216	9	US-09-925-299-841	Sequence 841, Appl1

ALIGNMENTS

RESULT 1
US-09-992-598-266
Sequence 266, Application US/09992598
Patent No. US20020160384A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992, 598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13

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Db 117 WRKCV 121

Db 117 WRKCV 121

RESULT 15
AAU80115
ID AAU80115 standard; Protein; 121 AA.Search completed: March 10, 2003, 17:38:44
Job time : 31.1622 secs

AC AAU80115;

DT 07-OCT-2002 (first entry)

DE pig sensory epithelium neuropeptide-like receptor (SENR) protein.

KW SENR: Sensory epithelium neuropeptide-like receptor; pig; fear;
attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
schizophrenia; G protein-coupled; receptor.

OS Sus scrofa.

PN WO200214513-A1.

PD 21-FEB-2002.

PF 10-AUG-2001; 2001WO-JP06899.

PR 10-AUG-2000; 2000JP-0247968.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Matsumoto Y, Watanabe T, Takahashi H, Mori M;

DR WPI; 2002-329576/36.

PT Polypeptide GPR12 with ligand activity to sensor epithelium
neuropeptide-like receptor, useful e.g. in treating attention deficit
disorder or narcolepsy, or for screening drug candidates for these
indications and for anxiety

PS Claim 6; Page 271; 290pp; Japanese.

CC This invention relates to an anti-attention deficit disorder or anti-
CC narcolepsy agent containing a polypeptide with a sequence identical or
CC substantially similar to a fully defined 12 amino acid sequence given in
CC the specification, and its amide, ester or their salt. The peptides
CC have ligand activity to sensory epithelium neuropeptide-like receptor
CC (SENR) protein. The invention also includes a method for diagnosing
CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
CC schizophrenia or fear. The polypeptides of the invention, their
CC precursor proteins and their encoding DNAs are useful in treating
CC attention deficit disorder or narcolepsy, or for screening drug
CC candidates for these indications and for anxiety, depression, insomnia,
CC schizophrenia or fear. They are also useful for gene therapy. The
CC polypeptide is a G protein-coupled receptor protein, with ligand
CC activity to sensor epithelium neuropeptide-like receptor. The present
CC sequence represents a pig sensory endothelium neuropeptide-like receptor
CC protein of the invention.

SQ Sequence 121 AA;

Query Match 52.3%; Score 342.5; DB 23; Length 121;

Best Local Similarity 61.6%; Pred. No. 1.5e-32; Mismatches 31; Indels 5; Gaps 4;

Matches 77; Conservative 12; Mismatches 31; Indels 5; Gaps 4;

OY 1 MYKLASCCLFIFGLNPLSLPLDLSREISFQSDAPHEADRLTPEETERASLIQILPEML 60

DB 1 MSKLVLP-CLLLLCGLGLFALPVPDSRKEPLPSAP-EDVRSAMDELERASLIQMLPETP 58

OY 61 GAERGDILRKADSSNIFNRGNLRKRFODFSGDDPNILSLHLARIWKPKKRETP-DCF 119

DB 59 GAEAGEDLRFADAGMDIFRYRGEMRK-AFSGDPNIFLSHLARIKKPKKRGPSSECF 116

OY 120 WRKCV 124

|||||

OY 120 WKYCV 124
 |||||
 Db 118 WKYCV 122

RESULT 13

AAU80120
 ID AAU80120 standard; Protein: 122 AA.

AC AAU80120;

DT 07-OCT-2002 (first entry)

DE Cow sensory epithelium neuropeptide-like receptor (SENR) protein.

KW SENR: Sensory epithelium neuropeptide-like receptor; cow; fear;
 attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
 schizophrenia; G protein-coupled; receptor.

OS Bos taurus.

PN W0200214513-A1.

PD 21-FEB-2002.

PF 10-AUG-2001; 2001WO-JP06899.

PR 10-AUG-2000; 2000JP-0247968.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Matsumoto Y, Watanabe T, Takahashi H, Mori M;

WPI: 2002-329576/36.

PT Polypeptide GPR12 with ligand activity to sensor epithelium
 neuropeptide-like receptor, useful e.g. in treating attention deficit
 disorder or narcolepsy, or for screening drug candidates for these
 indications and for anxiety

PS Claim 6; Page 276; 290pp; Japanese.

CC This invention relates to an anti-attention deficit disorder or anti-
 narcolepsy agent containing a polypeptide with a sequence identical or
 CC substantially similar to a fully defined 12 amino acid sequence given in
 CC the specification, and its amide, ester or their salt. The peptides
 CC have ligand activity to sensory epithelium neuropeptide-like receptor
 CC (SENR) protein. The invention also includes a method for diagnosing
 CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
 CC schizophrenia or fear. The polypeptides of the invention, their
 CC precursor proteins and their encoding DNAs are useful in treating
 CC attention deficit disorder or narcolepsy, or for screening drug
 CC candidates for these indications and for anxiety, depression, insomnia,
 CC schizophrenia or fear. They are also useful for gene therapy. The
 CC polypeptide is a G protein-coupled receptor protein, with ligand
 CC activity to sensor epithelium neuropeptide-like receptor. The present
 CC sequence represents the cow sensory endothelium neuropeptide-like
 CC receptor protein of the invention.

SO Sequence 122 AA;

Query Match 61.4%; Score 402; DB 23; Length 122;
 Best Local Similarity 68.8%; Pred. No. 1.4e-39;
 Matches 86; Conservative 10; Mismatches 25; Indels 4; Gaps 3;

OY 1 MYKLASCCLFIFGLNPLSLPLDSREISFQLSAPHEADRLPPELEFRASLLQIIPML 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MYKLAVSCCLFISLNPPLSLPLVDSRQESLQLLAP-EDVRSTLDELERSLLQMLPEMS 59
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 61 GAERGDLRKADSTNIFNPRGNLRKFQDFSGODPNILSHLLARIMKPKR-EPDPCF 119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 60 GAETGGLRMTDPTNIFPRGNMRK--AFSGODPKLFLSDLSLRIRKOSKKRGPSECF 117
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY 120 WKYCV 124
 |||||
 Db 118 WKYCV 122

RESULT 14

AAB12496
 ID AAB12496 standard; Protein: 121 AA.

AC AAB12496;

DT 27-OCT-2000 (first entry)

DE Pig SENR ligand protein sequence SEQ ID NO:18.

KW SENR: Sensory epithelium neuropeptide-like receptor; urotenensin II;
 diagnosis; G protein-coupled receptor; hypertension; GPR14; hormone;
 kidney disease; regulator; central function; circulatory function;
 heart function; immune system function; digestive function;
 metabolic function; genital function.

OS Sus scrofa.

PN W0200032627-A1.

PD 08-JUN-2000.

PF 29-NOV-1999; 99WO-JP06649.

PR 30-NOV-1998; 98JP-0338984.

PR 04-FEB-1999; 99JP-0026848.

PR 26-AUG-1999; 99JP-0239367.

PA (TAKE) TAKEDA CHEM IND LTD.

PI Mori M, Abe M, Shimomura Y, Sugo T, Kitada C;

WPI: 2000-412287/35.

PT Urotenensin peptides which are ligands for sensory epithelium
 neuropeptide-like receptor (SENR) for diagnosis and treatment of
 hypertension

PS Claim 4; Page 134; 147pp; Japanese.

CC The present invention provides peptides which are ligands for sensory
 CC epithelium neuropeptide-like receptor (SENR), and their amides, esters
 CC and salts. SENR is a G-protein coupled receptor protein (also known as
 CC GPR14), and the peptides which are ligands for it are forms of the
 CC peptide hormone urotenensin II. The peptides can be used in the treatment
 CC and diagnosis of hypertension and kidney disease, and the development of
 CC drugs which are regulators of central functions, circulatory functions,
 CC heart functions, immune system functions, digestive functions, metabolic
 CC functions and genital functions. The present sequence represents a
 CC specifically claimed pig SENR ligand protein sequence, from the
 CC present invention.

SO Sequence 121 AA;

Query Match 52.3%; Score 342.5; DB 21; Length 121;
 Best Local Similarity 61.6%; Pred. No. 1.5e-32;
 Matches 77; Conservative 12; Mismatches 31; Indels 5; Gaps 4;

OY 1 MYKLASCCLFIFGLNPLSLPLDSREISFQLSAPHEADRLPPELEFRASLLQIIPML 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1 MSKLTVP-CLLLCCLGLFALPVPDSRKEPLPSAP-EDVRSMDELERSLLQMLPETP 58
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 61 GAERGDLRKADSTNIFNPRGNLRKFQDFSGODPNILSHLLARIMKPKR-EPDPCF 119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 59 GAEGEDLRADAGMDIFPRGEMRK--AFSGODPNILSHLLARIMKPKRGPSECF 116
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 OY 120 WKYCV 124
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

XX	DE	Human Urotensin II partial polypeptide sequence.
XX	KW	Urotensin II: systemic vasoconstrictor; antihypertensive; agonist; antagonist;
XX	KM	myocardial contractile dysfunction; lethal arrhythmia; asthma; allergy;
XX	KM	ischemic coronary artery disease; atherosclerosis; metabolic disease;
XX	KM	restenosis; hypertension; hypotension; pulmonary disease; cancer;
XX	KM	cerebrovascular event; neurogenic inflammation; migraine; pain;
XX	KM	autoimmune disease; fibroproliferative disorder; renal failure;
XX	KW	microbial infection; viral infection; eating disorder;
XX	KM	Huntington's disease; Gilles de la Tourette's syndrome.
XX	OS	Homo sapiens.
XX	FI	Key Location/Qualifiers
XX	FI	CDS 4..315
XX	FT	/*tag= a
XX	FT	/product= Human_Urotensin_II
XX	PN	W0935266-A2.
XX	PD	15-JUL-1999.
XX	PF	08-JAN-1999; 99W0-US00489.
XX	XX	09-JAN-1998; 98US-0072383.
XX	PR	04-FEB-1998; 98US-0073616.
XX	PR	20-FEB-1998; 98US-0027381.
XX	PR	05-JAN-1999; 99US-0225747.
XX	PA	(SMIK) SMITHKLINE BEECHAM CORP.
XX	PA	(SMIK) SMITHKLINE BEECHAM PLC.
XX	PA	(SMIK) SMITHKLINE BEECHAM LAB PHARM.
XX	PI	Culp JS, McNulty DE, Ellis CE, Douglas SA, Willecke RN, Aiyar NV;
XX	PI	Arnold AR, Khandoudi N, Gout B, Al-Barazangi K;
XX	DR	WPI: 1999-590681/50.
XX	DR	N-PSDB: AA28382.
XX	PT	New human Urotensin II polypeptides and polynucleotides -
XX	PS	Claim 14; Page 28; 39pp: English.
XX	CC	This is a partial human Urotensin II polypeptide sequence. This sequence
XX	CC	was identified prior to the identification of the full length sequence
XX	CC	AA28381. This partial sequence was derived from EST (Expressed Sequence
XX	CC	Tag) sequences. Urotensin II is the most potent mammalian
XX	CC	vasoconstrictor identified to date. The invention relates to Urotensin II
XX	CC	antibodies specific for Urotensin II. The polypeptides and
XX	CC	polynucleotides of the invention can be used to identify agonists and
XX	CC	antagonists of the Urotensin II polypeptide. Urotensin II induces
XX	CC	systemic vasoconstriction, myocardial contractile dysfunction, and
XX	CC	ultimately, lethal arrhythmias. Urotensin polypeptides and
XX	CC	polynucleotides, agonists, antagonists and antibodies are used to treat
XX	CC	diseases, including ischemic coronary artery disease; atherosclerosis;
XX	CC	metabolic diseases; CHF/myocardial dysfunction; arrhythmias; restenosis;
XX	CC	hypertension; hypotension; pulmonary disease; fibrotic vasculopathies;
XX	CC	cerebrovascular events; neurogenic inflammation/migraine; hematopoietic
XX	CC	disorders; cancer; autoimmune diseases; fibroproliferative disorders;
XX	CC	renal failure and glomerulopathies; microbial and viral infections; pain;
XX	CC	eating disorders; asthma; allergies; Huntington's disease or Gilles de la
XX	CC	Tourette's syndrome. The polynucleotide is also useful as a source of
XX	CC	primers and probes, and also for detecting the above diseases.
XX	XX	Sequence 103 AA:
XX	XX	Query Match 76.0%; Score 498; DB 20; Length 103;
XX	XX	Best Local Similarity 87.3%; Pred. No. 4.6e-51;
XX	XX	Matches 96; Conservative 2; Mismatches 4; Indels 8; Gaps 1;
XX	XX	15 LNPILSLPLDLSSEISFQLSAPHEKDKRLPPELEFRSLQIQLPEMIGARGGILKRAQSS 74

```

Db      2 MNPTLS-----ICRYSAAPHEDALTFPEELERASLTGLDLPMLGAERGDILRKADSS 53
QY      75 TNIFNPRGNLRRFQDSGQDPNILLSHLARIMKPYKKRETPDCFMKYCY 124
          |||
          54 TNIFNPRGNLRRFQDSGQDPNILLSHLARIMKPYKKRETPDCFMKYCY 103

RESULT 12
AAB12501
ID      AAB12501 standard; Protein; 122 AA.
AC      AAB12501;
AD      27-OCT-2000 (first entry)
DE      Bovine SENR ligand protein sequence SEQ ID NO:29.
XX
XX      SENR; sensory epithelium neuropeptide-like receptor; urotensin II;
KW      diagnosis; G protein-coupled receptor; hypertension; GPR14; hormone;
KW      kidney disease; regulator; central function; circulatory function;
KW      heart function; immune system function; digestive function;
KW      metabolic function; genital function.
XX
XX      Bos taurus.
XX      WO200032627-A1.
XX      08-JUN-2000.
XX
XX      29-NOV-1999; 99WO-JP06649.
XX
XX      30-NOV-1998; 98JP-0338984.
XX      04-FEB-1999; 99JP-0026848.
XX      26-AUG-1999; 99JP-0239367.
XX
XX      (TAKE ) TAKEDA CHEM IND LTD.
XX
XX      Mori M, Abe M, Shlomura Y, Sugo T, Kitada C;
XX      WPI: 2000-412287/35.
XX
XX      Urotensin peptides which are ligands for sensory epithelium
XX      neuropeptide-like receptor (SENR) for diagnosis and treatment of
XX      hypertension
XX
XX      Example 36; page 140-141; 147pp; Japanese.
XX
XX      The present invention provides peptides which are ligands for sensory
XX      epithelium neuropeptide-like receptor (SENR), and their amides, esters
XX      and salts. SENR is a G-protein coupled receptor protein (also known as
XX      GPR14), and the peptides which are ligands for it are forms of the
XX      peptide hormone urotensin II. The peptides can be used in the treatment
XX      and diagnosis of hypertension and kidney disease, and the development of
XX      drugs which are regulators of central functions, circulatory functions,
XX      heart functions, immune system functions, digestive functions, metabolic
XX      functions and genital functions. The present sequence represents a
XX      bovine SENR ligand protein from the present invention.
XX
XX      Sequence 122 AA:
XX
QY      Query Match 61.4%; Score 402; DB 21; Length 122;
QY      Best Local Similarity 68.8%; Pred. No.1.4e-39;
QY      Matches 86; Conservative 10; MisMatches 25; Indels 4; Gaps 3.
Db      1 MYKLASCCILFTGFLNPLSLPLDSREISFOLSAFHEDARLTFPEELERASLTGLDLPML 60
          |||
          1 MYKLASCCILFTGSLNPLSLPLVDSRQSLQLAD-EDVRSITDLEERASLTGLDLPML 59
QY      61 GARGGILRKADSSNTNIFNPRGNLRRFQDSGQDPNILLSHLARIMKPYKKR-ETPDGF 119
          |||
          60 GALTGEGRLNRTDPTTNIFNPRGNMKR-AFSGQDPKFLSLDLSLRIRKQSKKRCPSSECF 117

```


OS	Homo sapiens.
XX	
PN	MO99353266.A2.9
XX	
PD	15-JUL-1999.
XX	
PF	08-JAN-1999; 99MO-US00489.
XX	
PR	09-JAN-1998; 98US-0072383.
PR	04-FEB-1998; 98US-0073616.
PR	20-FEB-1998; 98US-0027381.
PR	05-JAN-1999; 99US-0225747.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PA	(SMIK) SMITHKLINE BEECHAM LAB PHARM.
XX	
PI	Culp JS, McNulty DE, Ellis CE, Douglas SA, Willette RN, Aiyar NV,
PI	Arnold AR, Khandoudi N, Gout B, Al-barazanjli K,
XX	
DR	WPI: 1999-590681/50.
DR	N-PSDB; AA228381.
XX	
PT	New human Urotensin II polypeptides and polynucleotides -
XX	Claim 1, Page 28; 39pp; English.

This is the human urotensin II polypeptide I sequence. Urotensin II is the most potent mammalian vasoconstrictor identified to date. This sequence shows homology with carp urotensin II- α . The invention relates to urotensin II polypeptides and polynucleotides, which can be used to generate antibodies specific for urotensin II. The polypeptides and polynucleotides of the invention can be used to identify agonists and antagonists of the urotensin II polypeptide. Urotensin II induces systemic vasoconstriction, myocardial contractile dysfunction, and ultimately, lethal arrhythmias. Urotensin polypeptides and polynucleotides, agonists, antagonists and antibodies are used to treat diseases, including ischaemic coronary artery disease, atherosclerosis; metabolic diseases; CHF/myocardial dysfunction; arrhythmias; restenosis; hypertension; pulmonary disease; fibrotic vasculopathies; cerebrovascular events; neurogenic inflammation/migraine; haematopoietic disorders; cancer; autoimmune diseases, fibroproliferative disorders; renal failure and glomerulopathies; microbial and viral infections; pain; eating disorders; asthma; allergies; Huntington's disease or Gilles de la Tourette's syndrome. The polynucleotide is also useful as a source of primers and probes, and also for detecting the above diseases.

Query Match	81.5%;	Score 533.5;	DB 20;	Length 139;
Best Local Similarity	84.8%;	Pred. No. 4.3e-55;		
Matches 106; Conservative	2;	Mismatches 12;	Indels 5;	Gaps 2

```

QY      2 YKLAACCLLEFIFGFLNPLSLPLDLS--RETSPQLSAPHEDARLTPELEFRASLDIOLPEM 59
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      18 HKSTSLC---FGHNPSYSLPLHIDLLLELSFQLSAPHEDARLTPELEFRASLDIOLPEM 74
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      60 LGAERGDILIRKADSTNIENFRGNLRKFQDFQSGODNNILLSHLARIMKPYKKRTPPCF 115
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      75 LGAERGDILIRKADSTNIENFRGNLRKFQDFQSGODNNILLSHLARIMKPYKKRTPPCF 130
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      120 WKYCV 124
      : | | | | |
Db      135 WKYCV 139

```

RESULT 11	
AAV39391	
ID	AAV39391 standard; Protein; 103 AA
XX	
AC	AAV39391;
XX	
DT	20-DEC-1999 (first entry)

reaction, to generate transgenic animals or knock-out animals which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides are useful in gene therapy, and as molecular weight markers for protein electrophoresis purposes. The sequences may also be used to detect overexpression on PRO polypeptides in cancerous tumours and for screening for differentially expressed genes using microarray technology. The present sequence represents a human PRO protein of the invention.

Sequence 124 AA:

Query Match 99.2%: Score 650; DB 23; Length 124;
Best Local Similarity 99.2%: Pred. No. 5.8e-69;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYKLASCCLLFTGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60
DB 1 MYKLASCCLLFTGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60
QY 61 GAERGDILRKADSTNINFRGNLRRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFW 120
DB 61 GAERGDILRKADSTNINFRGNLRRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 8
AAU81965

ID AUA81965 standard; Protein: 124 AA.

XX AAU81965;

DT 09-APR-2002 (first entry)

DE Human PRO1068.

XX Human; PRO; antiinflammatory; ophthalmological; vasotropic;
XX retinal cell injury; ocular disease; retinitis pigmentosa;
XX macular degeneration; retinal detachment; retinal tear; retinopathy;
XX retinal degenerative disease; macular hole; degenerative myopia;
XX acute retinal necrosis syndrome; traumatic choriorretinopathy;
XX Purtscher's retinopathy; oedema; ischaemic condition;
XX retinal vision occlusion; collagen vascular disease;
XX thrombocytopaenic purpura; uveitis; retinal vasculitis; Fales disease;
XX systemic lupus erythematosus; environmental trauma.

OS Homo sapiens.

PN WO200109327-A2.

PD 08-FEB-2001.

PF 28-JUL-2000; 2000WO-US20710.

XX 28-JUL-1999; 99US-146222P.
XX 13-SEP-1999; 99WO-US20944.
XX 15-SEP-1999; 99WO-US21090.
XX 29-NOV-1999; 99WO-US28214.
XX 30-NOV-1999; 99WO-US28513.
XX 01-DEC-1999; 99WO-US28301.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 15-MAR-2000; 2000WO-US06884.
XX 30-MAR-2000; 2000WO-US08439.
XX 17-MAY-2000; 2000WO-US13705.

XX (GENTH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;

XX Kijavain II, Lafleur M, Mark MR, Masters SA, Pitti RM;

XX Watanabe CK, Wood WI;

XX MPI: 2002-130120/17.

XX N-PSDB: ABK28601.

XX Promoting survival of retinal cells, or delaying or preventing retinal

XX cell injury or death, by contacting retinal cells with PRO175, 220,

XX PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132

XX polypeptide -

XX Claim 44; Fig 27; 152pp: English.

XX The invention relates to promoting the survival of retinal cells, or
XX delaying or preventing retinal cell injury or death, by contacting the
XX retinal cells with the polypeptide such as PRO175, PRO220, PRO216,
XX PRO243, PRO306, PRO346, PRO322, PRO536, PRO943, PRO840, PRO828,
XX PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
XX encoding the PRO proteins, a vector comprising the nucleic acid, a host
XX cell comprising the vector, and anti-PRO antibody. The PRO proteins are
XX useful for promoting survival of retinal cells (retinal neurons such as
XX retinal ganglion cells, displaced retinal ganglion cells, amacrine
XX cells, displaced amacrine cells, horizontal neurons or bipolar neurons,
XX rod photoreceptors, or supportive cells such as Muller cells or pigment
XX epithelial cells), or delaying or preventing retinal cell injury or
XX death caused by ocular disease (which is or is associated with
XX retinitis pigmentosa, macular degeneration, retinal detachment, retinal
XX tear, retinopathy, retinal degenerative disease, traumatic
XX degenerative myopia, acute retinal necrosis syndrome, traumatic
XX choriorretinopathy or contusion, Purtscher's retinopathy, oedema, an
XX ischaemic condition, central or branch retinal vision occlusion,
XX collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal
XX vasculitis, occlusion associated with Fales disease or systemic lupus
XX erythematosus), retinal injury or environmental trauma. The retinal
XX cell injury or death is delayed or prevented by substantially not
XX causing angiogenesis or mitogenesis. The present sequence represents
XX a PRO protein.

XX Sequence 124 AA:

Query Match 99.2%: Score 650; DB 23; Length 124;
Best Local Similarity 99.2%: Pred. No. 5.8e-69;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MYKLASCCLLFTGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60
DB 1 MYKLASCCLLFTGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60
QY 61 GAERGDILRKADSTNINFRGNLRRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFW 120
DB 61 GAERGDILRKADSTNINFRGNLRRKFQDFSGQDPNILLSHLLARIWKPKKRETPDCFW 120
QY 121 KYCV 124
DB 121 KYCV 124

RESULT 9

ID AAY93640 standard; Protein: 104 AA.

XX AAY93640;

XX 25-SEP-2000 (first entry)

XX Amino acid sequence of a human pro-urotensin II (UII) polypeptide.

XX Urotensin II: motor neuron; hypertensive; neurodegeneration;

XX spinal cord trauma; hemi-plegia; para-plegia;

PR 30-NOV-1999; 99MO-US28313.
 PR 01-DEC-1999; 99MO-US28634.
 PR 09-DEC-1999; 99US-0170262.
 PR 20-DEC-1999; 99MO-US30911.
 PR 05-JAN-2000; 2000MO-US00219.
 PR 06-JAN-2000; 2000MO-US00376.
 PR 11-FEB-2000; 2000MO-US03565.
 PR 18-FEB-2000; 2000MO-US04341.
 PR 18-FEB-2000; 2000MO-US04342.
 PR 22-FEB-2000; 2000MO-US04414.
 PR 24-FEB-2000; 2000MO-US04914.
 PR 15-MAR-2000; 2000MO-US06884.
 PR 20-MAR-2000; 2000MO-US07377.
 PR 21-MAR-2000; 2000MO-US07532.
 PR 30-MAR-2000; 2000MO-US08439.
 PR 17-MAY-2000; 2000MO-US13705.
 PR 22-MAY-2000; 2000MO-US14042.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Chan B, Goddard A, Godowski PJ, Gurney AL;
 PI Hebert C, Henzel W, Kabakoff RC, Shelton DL, Tumas D, Watanabe CK;
 PI Wood WI;

DR WPI: 2001-025253/03.
 DR N-PSDB: AAC91478.

XX Thirty three nucleic acids encoding PRO polypeptides which are useful
 PT in the diagnosis and treatment of immune related disorders, e.g.
 PT systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 PT thyroiditis and diabetes mellitus -

XX Claim 58; Fig 36; 218pp; English.

XX The present sequence is one of thirty three novel PRO polypeptides.
 CC The PRO polypeptides, anti-PRO antibodies, agonists and
 CC antagonists are useful for treating and diagnosing immune related
 CC disorders such as systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems (such as multiple sclerosis, idiopathic
 CC demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic
 CC inflammatory demyelinating polyneuropathy), hepatobiliary diseases
 CC (such as infectious, autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis and sclerosing cholangitis),
 CC inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's
 CC disease, autoimmune or immune-mediated skin diseases (such as bullous
 CC skin diseases, erythema multiforme, contact dermatitis, psoriasis),
 CC allergic diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC food hypersensitivity and urticaria), immunological diseases of the
 CC lung (such as eosinophilic pneumonias, idiopathic pulmonary fibrosis
 CC and hypersensitivity pneumonitis), transplantation associated diseases
 CC including graft rejection and graft-versus-host diseases.

XX Sequence 124 AA;

Query Match 99.2%; Score 650; DB 22; Length 124;
 Best Local Similarity 99.2%; Pred. No. 5.8e-69;
 Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MYKLASCLLFTGLFNLPLSLPLDSREISFQLSAPHEDARLPPELEERSLQIIPPEML 60
 DB 1 MYKLASCLLFTGLFNLPLSLPLDSREISFQLSAPHEDARLPPELEERSLQIIPPEML 60
 OY 61 GAERGDLRKADSSSTNIFNRGNLRFQDSGDPNTLLSHLARIMKPKKRETPCCFW 120
 DB 61 GAERGDLRKADSSSTNIFNRGNLRFQDSGDPNTLLSHLARIMKPKKRETPCCFW 120
 OY 121 KYCV 124
 IIII

Db 121 KYCV 124

RESULT 7
 ABG34042
 ID ABG34042 standard; Protein; 124 AA.

XX ABG34042;

DT 15-JUL-2002 (first entry)

DE Human Pro peptide #13.

XX Human; PRO; secreted protein; transmembrane protein;
 KW genetic disorder; tumour; cancer.

OS Homo sapiens.

XX WO200224888-A2.

XX 28-MAR-2002.

PE 29-AUG-2001; 2001MO-US27099.

XX 01-SEP-2000; 2000US-229896P.
 PR 05-SEP-2000; 2000US-230621P.
 PR 22-SEP-2000; 2000US-235147P.
 PR 10-NOV-2000; 2000MO-US30873.
 PR 12-JAN-2001; 2001US-261878P.
 PR 16-JAN-2001; 2001US-261910P.
 PR 16-JAN-2001; 2001US-261939P.
 PR 16-JAN-2001; 2001US-262150P.
 PR 25-JAN-2001; 2001US-264395P.
 PR 02-FEB-2001; 2001US-26421P.
 PR 09-FEB-2001; 2001US-267623P.
 PR 28-FEB-2001; 2001MO-US06520.
 PR 09-MAR-2001; 2001US-274399P.
 PR 03-APR-2001; 2001US-280982P.
 PR 04-APR-2001; 2001US-282129P.
 PR 04-APR-2001; 2001US-282199P.
 PR 09-MAY-2001; 2001US-290589P.
 PR 25-MAY-2001; 2001MO-US17092.
 PR 01-JUN-2001; 2001MO-US17800.
 PR 20-JUN-2001; 2001MO-US19692.
 PR 29-JUN-2001; 2001MO-US21066.
 PR 09-JUL-2001; 2001MO-US21735.

XX (GETH) GENENTECH INC.

XX Baker KP, Eaton DL, Filvaroff E, Grimaldi JC;
 PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
 PI Fong S;

DR WPI: 2002-362426/39.
 DR N-PSDB: ABB69973.

XX New PRO polypeptides and polynucleotides encoding the polypeptides,
 PT useful in gene therapy, chromosome identification, tissue typing, or
 PT for genetic analysis of individuals with genetic disorders -
 XX Claim 11; Figure 26; 218pp; English.

XX This invention relates to the cDNA and protein sequences of novel
 CC secreted and transmembrane polypeptides PRO polypeptides. The
 CC invention also comprises a method for producing the proteins of the
 CC invention by recombinant means and antibodies specific for the protein
 CC of the invention. The antibody may be used to detect the PRO
 CC proteins of the invention and may be used to modify their activity.
 CC polynucleotides may be used as hybridisation probes for a cDNA library
 CC to isolate the full-length PRO cDNA or to isolate other cDNAs, to
 CC construct hybridisation probes for mapping the gene which encodes that
 CC PRO and for genetic analysis of individuals with genetic disorders, in
 CC assays to identify other proteins or molecules involved in binding

Best Local Similarity 99.2%; Pred. No. 5.8e-69;
Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MYKLASCCLLFGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60
Db 1 MYKLASCCLLFGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60

Oy 61 GAERGDILRKADSSNTINFPNGNLKRFQDFSGQDPNILLSHLARIWKPKKRETPDCFW 120
Db 61 GAERGDILRKADSSNTINFPNGNLKRFQDFSGQDPNILLSHLARIWKPKKRETPDCFW 120

Oy 121 KYCV 124
Db 121 KYCV 124

RESULT 5

AAB65230

AAB65230 standard; Protein: 124 AA.

AC AAB65230;

DT 02-APR-2001 (first entry)

DE Human PRO1068 (UNQ525) protein sequence SEQ ID NO:266.

KW Human; secreted and transmembrane protein; PRO; cytosolic;
cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
diagnostic assay.

OS Homo sapiens.

PN WO200073454-A1.

PD 07-DEC-2000.

PF 30-MAR-2000; 2000MO-US08439.

XX 02-JUN-1999; 99MO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149396.
PR 15-SEP-1999; 99MO-US21090.
PR 15-SEP-1999; 99MO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99MO-US28313.
PR 01-DEC-1999; 99MO-US28301.
PR 16-DEC-1999; 99MO-US30095.
PR 20-DEC-1999; 99MO-US30911.
PR 05-JAN-2000; 2000MO-US00219.
PR 06-JAN-2000; 2000MO-US00376.
PR 11-FEB-2000; 2000MO-US03565.
PR 18-FEB-2000; 2000MO-US04341.
PR 22-FEB-2000; 2000MO-US04414.
PR 24-FEB-2000; 2000MO-US04914.
PR 24-FEB-2000; 2000MO-US05004.
PR 02-MAR-2000; 2000MO-US05841.
PR 15-MAR-2000; 2000MO-US06884.
PR 20-MAR-2000; 2000MO-US07377.

PA (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
PI Ferrara N, Fong S, Gether H, Geirtsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;

WPI: 2001-032160/04.

DR N-PSDB; AAF44193.

XX PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -
XX
PS Claim 12; Fig 184; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytosolic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.

SQ Sequence 124 AA;

Query Match 99.2%; Score 650; DB 22; Length 124;

Best Local Similarity 99.2%; Pred. No. 5.8e-69;

Matches 123; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 MYKLASCCLLFGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60
Db 1 MYKLASCCLLFGFLNPLSLPLDLSREISFQLSAPHEDARLTPEELERASLLQILPEML 60

Oy 61 GAERGDILRKADSSNTINFPNGNLKRFQDFSGQDPNILLSHLARIWKPKKRETPDCFW 120
Db 61 GAERGDILRKADSSNTINFPNGNLKRFQDFSGQDPNILLSHLARIWKPKKRETPDCFW 120

Oy 121 KYCV 124
Db 121 KYCV 124

RESULT 6

AAB50919

AAB50919 standard; Protein: 124 AA.

AC AAB50919;

DT 21-MAR-2001 (first entry)

DE Human PRO1068 protein.

KW Human; PRO; antiinflammatory; dermatological; antirheitic;
KW antineumatic; cardiant; antianaemic; immunosuppressive; antihypoid;
KW antidiabetic; nootropic; neuroprotective; hepatotropic; vituicide;
KW anti-allergic; antistatic; immune related disorder;
KW hepatobiliary disease; autoimmune disease; allergy.

OS Homo sapiens.

PN WO200073452-A2.

PD 07-DEC-2000.

PF 02-JUN-2000; 2000MO-US15264.

XX 02-JUN-1999; 99MO-US12252.
PR 20-JUL-1999; 99US-0144732.
PR 20-JUL-1999; 99US-0144758.
PR 28-JUL-1999; 99US-0146222.
PR 01-SEP-1999; 99MO-US20111.
PR 15-SEP-1999; 99MO-US21090.
PR 15-SEP-1999; 99MO-US21547.
PR 29-OCT-1999; 99US-0162506.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW pharmaceutical; receptor Immunoadhesin; gene mapping.
XX Homo sapiens.
OS MO9963088-A2.
XX
XX
PD 09-DEC-1999.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 11-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 18-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 19-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 23-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 24-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.

PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 25-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090699.
PR 25-JUN-1998; 98US-0090722.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.

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XX 26-NOV-1999: 99MO-FR02941.
PF
XX
XX 26-NOV-1999: 98FR-0014914.
PR
XX
XX (INRM ) INST NAT SANTE & RECH MEDICALE.
PA
XX Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H:
PI
XX WPI: 2000-400075/34.
DR
XX N-PSDB: AAA46698.
PT
XX New mammalian urotensin II polypeptide, useful for treating
PT neurodegeneration and spinal cord injury -
XX
XX Claim 2: Fig 2: 42pp: French.
PS
XX
XX The present sequence represents a human prepro-urotensin II polypeptide.
CC In mammals, urotensin II promotes survival and regeneration of motor
CC neurons, and also has a hypertensive effect. The urotensin II
CC polypeptides and polynucleotides are useful for treating
CC neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
CC paraplegia or amyotrophic lateral sclerosis). The polypeptides
CC are also used to screen for specific inhibitors, i.e. potential
CC antihypertensive agents.
XX
XX Sequence 124 AA:
SQ
Query Match 100.0%; Score 655; DB 21; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.5e-69;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYKLASCLLFIQFLNPLSLPLDSREISFQLSAPHEEARLPPELERASLQIPEML 60
DB 1 MYKLASCLLFIQFLNPLSLPLDSREISFQLSAPHEEARLPPELERASLQIPEML 60
QY 61 GAERGDLIRKADSTNIFNPGNLRKRFQDFSGODPNILSLHLARIWKPKKRETPDCF 120
DB 61 GAERGDLIRKADSTNIFNPGNLRKRFQDFSGODPNILSLHLARIWKPKKRETPDCF 120
QY 121 KYCV 124
DB 121 KYCV 124
DB 121 KYCV 124
DE
RESULT 2
AA87319
ID AAY87319 standard; Protein: 124 AA.
XX
XX AAY87319;
XX
XX 11-MAY-2000 (first entry)
DE
XX Human signal peptide containing protein HSP-96 SEQ ID NO:96.
XX
XX Human: signal peptide-containing protein: HSP; diagnosis: cancer;
XX inflammation: cardiovascular disease; anticancer: anti-inflammatory;
XX antimicrobial: neurotropic; neuroprotective: cardiovascular; hepatotropic;
XX antitubercular: gene therapy; cell proliferation; neurological disorder;
XX reproductive disorder; developmental disorder; arteriosclerosis;
XX cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
XX asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
XX Parkinson's disease; Huntington's diseases; ovulatory defect;
XX muscular dystrophy.
XX
XX Homo sapiens.
XX
XX OS
XX PN
XX MO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX PD
XX 25-JUN-1999; 99MO-US14484.
XX
XX
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PR 26-JUN-1998: 98US-0090762.
PR 31-JUL-1998: 98US-0094983.
PR 01-OCT-1998: 98US-0102886.
PR 11-DEC-1998: 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KU, Baughn MR;
PI
PI Akerdlom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI: 2000-160673/14.
DR
XX N-PSDB: AA298204.
PT
XX
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease -
XX
XX Claim 1: Page 221-222: 327pp: English.
PS
XX
XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
CC neuroprotective, cardiovascular and antitubercular activities, and can
CC be used in gene therapy. HSPPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis), acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribozyme therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.
XX
XX Sequence 124 AA:
SQ
Query Match 100.0%; Score 655; DB 21; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.5e-69;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYKLASCLLFIQFLNPLSLPLDSREISFQLSAPHEEARLPPELERASLQIPEML 60
DB 1 MYKLASCLLFIQFLNPLSLPLDSREISFQLSAPHEEARLPPELERASLQIPEML 60
QY 61 GAERGDLIRKADSTNIFNPGNLRKRFQDFSGODPNILSLHLARIWKPKKRETPDCF 120
DB 61 GAERGDLIRKADSTNIFNPGNLRKRFQDFSGODPNILSLHLARIWKPKKRETPDCF 120
QY 121 KYCV 124
DB 121 KYCV 124
DB 121 KYCV 124
DE
RESULT 3
AAY6707
ID AAY6707 standard; Protein: 124 AA.
XX
XX AAY6707;
XX
XX 05-APR-2000 (first entry)
XX
XX DT
XX 25-APR-2000 (first entry)
XX
XX Membrane-bound protein PRO1068.
DE
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:24:52 ; Search time 30.1622 Seconds

(without alignments)
547.808 Million cell updates/sec

Title: US-09-831-907A-1

Perfect score: 655

Sequence: 1 MYKLASCCLEFLGFLNPLLS.....RIMKPKRREPPDCWKYCV 124

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	655	100.0	124	21	AAV87319
3	650	99.2	124	21	AAV66707
4	650	99.2	124	22	AAAB20118
5	650	99.2	124	22	AAAB65230
6	650	99.2	124	22	AAAB50919
7	650	99.2	124	23	ABG34042
8	650	99.2	124	23	AAU81965
9	549	83.8	104	21	AAV93640
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11	498	76.0	103	20	AAV93931	Human Urotensin II
12	402	61.4	122	21	AAAB12501	Bovine SENS IIlgand
13	402	61.4	122	23	AAU80120	Cow sensory epithe
14	342.5	52.3	121	21	AAAB12496	Pig SENS IIlgand pr
15	342.5	52.3	121	23	AAU80115	Pig sensory epithe
16	286.5	43.7	123	21	AAV93647	Amino acid sequenc
17	286.5	43.7	123	22	AAAB60445	Amino acid sequenc
18	286.5	43.7	123	23	AAU80124	Mouse urotensin II
19	282.5	43.1	123	21	AAV93644	Mouse urotensin II
20	282.5	43.1	123	22	AAAB60442	Amino acid sequenc
21	282.5	43.1	123	23	AAU80121	Rat urotensin II-1
22	215.5	32.9	85	21	AAAB12497	Pig SENS IIlgand pr
23	215.5	32.9	85	23	AAU80116	Pig sensory epithe
24	213.5	32.6	103	21	AAV93648	Amino acid sequenc
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26	79.5	12.1	543	22	ABAB64811	Drosophila melanog
27	79	12.1	3726	22	ABAB63947	Drosophila melanog
28	76	11.6	484	14	AAAB44751	Osteogenic fusion
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31	75	11.5	389	21	AAAG42055	Arabidopsis thalia
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36	74.5	11.4	328	21	AAAG49493	Arabidopsis thalia
37	74.5	11.4	389	21	AAAG49492	Arabidopsis thalia
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40	74.5	11.4	534	21	AAAG32972	Arabidopsis thalia
41	74	11.3	11	20	AAV93932	Mature human uroce
42	74	11.3	11	21	AAAB12469	Human SENS IIlgand
43	74	11.3	11	21	AAV93641	Amino acid sequenc
44	74	11.3	11	22	AAE02880	Urotensin-II pepti
45	74	11.3	11	22	AAV97703	Rat Urotensin II r

ALIGNMENTS

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AAV93639	
ID	AAV93639 standard; Protein; 124 AA.
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AC	AAV93639;
XX	
DT	25-SEP-2000 (first entry)
XX	
DE	Amino acid sequence of a human prepro-urotensin II (U1) polypeptide.
XX	
KW	urotensin II; motor neuron; hypertensive; neurodegeneration;
KW	spinal cord trauma; hemi-plegia; para-plegia;
KW	amyotrophic lateral sclerosis; antihypertensive agent.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
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FT	/note="signal peptide"
FT	21..110
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FT	Misc-difference
FT	46
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FT	Misc-difference
FT	47
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FT	Misc-difference
FT	81
FT	/note="encoded by ATG"
FT	Peptide
FT	114..124
FT	/note="urotensin II"
PN	WO200031265-A1.
PD	02-JUN-2000.

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Job time : 12.3946 secs

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,699A
FILING DATE: 24-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,023
FILING DATE: 01-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK-001CP6CN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-699A-15

Query Match 10.5%; Score 69; DB 2; Length 408;
Best Local Similarity 25.2%; Pred. No. 5.3;
Matches 34; Conservative 15; Mismatches 50; Indels 36; Gaps 5;

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DB 126 PRYHNHREFRDLKIPGCAVTAEFRIYKDYIRERFDNETFRISYQVQLQENHGRESDL 185
QY 62 -----AERGDILRKADSSIN--IFNPRGNL---RKFDPSGDDPMLLSHLARI 106
DB 186 FLDSRTLMASEGMLVFDTITATSNHVVNPRNHLGLQLSVETLDGOSINPKLAGLIGR- 244
QY 107 WKPYKKRETPDCFWK 121
DB 245 HGFONKOPFMVAFFK 259

RESULT 15
US-07-841-646-2
Sequence 2, Application US/07841646
Patent No. 5266683
GENERAL INFORMATION:
APPLICANT: OPPERMAN, HERMANN
APPLICANT: OZKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 616,374
FILING DATE: 21-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 600,024
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-841-646-2

Query Match 10.5%; Score 69; DB 1; Length 431;
Best Local Similarity 25.2%; Pred. No. 5.7;
Matches 34; Conservative 15; Mismatches 50; Indels 36; Gaps 5;

QY 22 PLDSREISFQLSAPHEDARLTPEELE-----RASLQILPEMIG----- 61
DB 149 PRYHNHREFRDLKIPGCAVTAEFRIYKDYIRERFDNETFRISYQVQLQENHGRESDL 208
QY 62 -----AERGDILRKADSSIN--IFNPRGNL---RKFDPSGDDPMLLSHLARI 106
DB 209 FLDSRTLMASEGMLVFDTITATSNHVVNPRNHLGLQLSVETLDGOSINPKLAGLIGR- 267
QY 107 WKPYKKRETPDCFWK 121
DB 268 HGFONKOPFMVAFFK 282


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Patent NO. 5266683
GENERAL INFORMATION:
APPLICANT: OPERMANN, HERMANN
APPLICANT: OZKAYINAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H. L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/841,646
FILING DATE: 19920221
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,968
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 579,865
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 569,920
FILING DATE: 20-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 483,913
FILING DATE: 22-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 422,613
FILING DATE: 17-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
REGISTRATION NUMBER: 27,829

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? REFERENCE/DOCKET NUMBER: CRP-001CP6
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: 617/248-7000
?   TELEFAX: 617/248-7100
?   INFORMATION FOR SEQ ID NO: 15:
?     SEQUENCE CHARACTERISTICS:
?       LENGTH: 408 amino acids
?       TYPE: AMINO ACID
?       TOPOLOGY: linear
?     MOLECULE TYPE: protein
US-07-841-646-15

Query Match      10.5%: Score 69; DB 1; Length 408;
Best Local Similarity 25.2%; Pred. No. 5.3;
Matches 34; Conservative 15; Mismatches 50; Indels 36; Gaps 5;

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RESULT 11
US-08-147-023-15
Sequence 15, Application US/08147023
Patent No. 3468845
GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OKAYNAK, ENGIN
APPLICANT: KUBERASAMPATH, THANGAVEL
APPLICANT: RUEGER, DAVID C.
APPLICANT: PANG, ROY H.L.
TITLE OF INVENTION: OSTEOGENIC DEVICES
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSEE: TESTA, NURWITZ & THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,023
FILING DATE: 21-FEB-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 810,560
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 827,052
FILING DATE: 28-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 660,162
FILING DATE: 22-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,988
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 621,849
FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:

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NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/232,857
FILING DATE: 15-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/789,354
FILING DATE: 27-JAN-1997
APPLICATION NUMBER: 60/074,075
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 09/058,725
FILING DATE: 10-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-50005-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-232-857-5

Query Match 11.3%; Score 74; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 ETPDCFWKVCV 124
Db 1 ETPDCFWKVCV 11

RESULT 8
US-09-477-071-5
; Sequence 5, Application US/09477071
; Patent No. 6348585
; GENERAL INFORMATION:
; APPLICANT: CULP, JEFFREY
; APPLICANT: MCNULTY, DEAN
; APPLICANT: ELLIS, CATHERINE
; TITLE OF INVENTION: HUMAN UROTENSIN II
; FILE REFERENCE: GP-70366-D2
; CURRENT APPLICATION NUMBER: US/09/477,071
; CURRENT FILING DATE: 2000-01-03
; EARLIER APPLICATION NUMBER: 09/027,381
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/072,383
; EARLIER FILING DATE: 1998-01-09
; EARLIER APPLICATION NUMBER: 60/073,616
; EARLIER FILING DATE: 1998-02-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 11
; TYPE: PRT

ORGANISM: HOMO SAPIENS
US-09-477-071-5

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Best Local Similarity 100.0%; Pred. No. 0.01;
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Db 1 ETPDCFWKVCV 11

RESULT 9
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; Sequence 10, Application US/07764731B
; Patent No. 5366875
; GENERAL INFORMATION:
; APPLICANT: Rosen, Vicki A.
; APPLICANT: Wang, Elizabeth A.
; APPLICANT: Wozney, John M.
; TITLE OF INVENTION: Methods for Producing BMP-7 Proteins
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Legal Affairs, Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/764,731B
; FILING DATE: 19910924
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kapinos, Ellen J.
; REGISTRATION NUMBER: 32,245
; REFERENCE/DOCKET NUMBER: G15159B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-876-1170
; TELEFAX: 617-876-5851
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-764-731B-10

Query Match 10.5%; Score 69; DB 1; Length 400;
Best Local Similarity 25.2%; Pred. No. 5.2;
Matches 34; Conservative 15; Mismatches 50; Indels 36; Gaps 5;

QY 22 PILDSEISFOLSAHPEDARLTPELE-----RASLQIIPMG----- 61
Db 118 PRYHRRERFPLSKPEEAVTAFAFRKYIRERFNETFRISYGVVLOEHGRESDL 177
QY 62 -----AERDILKKADSSTN--TFNRGNL---RFQDFSGDDPNILLSHLLARI 106
Db 178 FLDSRTLMASEGWLVDIATSNHWVVRHNLGLQSVETLDGOSINPKLAGLIGR- 236
QY 107 WKPYKKRTPDCFWK 121
Db 237 HGPONKOPFWAFAFR 251

RESULT 10
US-07-841-646-15
; Sequence 15, Application US/07841646

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: March 10, 2003, 17:37:08 ; Search time 11.3946 seconds
(without alignments)
320.191 Million cell updates/sec

Title: US-09-831-907A-1
Perfect score: 655
Sequence: 1 MYKASCCLEFIFGLNLLS.....RIMKPKRKREPPDCFMKVCV 124

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.AA:*
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2: /cgn2_6/plodata/2/1aa/5B.COMB.pep:*
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5: /cgn2_6/plodata/2/1aa/PCtUS.COMB.pep:*
6: /cgn2_6/plodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	74	11.3	11 3 US-09-027-381-5	Sequence 5, Appl1
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8	74	11.3	11 4 US-09-477-071-5	Sequence 5, Appl1
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19	69	10.5	431 1 US-08-206-864-2	Sequence 2, Appl1
20	69	10.5	431 1 US-08-278-729A-17	Sequence 17, Appl1
21	69	10.5	431 1 US-08-480-528A-4	Sequence 4, Appl1
22	69	10.5	431 1 US-08-479-666-4	Sequence 4, Appl1
23	69	10.5	431 1 US-08-155-343A-17	Sequence 17, Appl1
24	69	10.5	431 1 US-08-406-672-17	Sequence 17, Appl1
25	69	10.5	431 1 US-08-643-563A-17	Sequence 17, Appl1
26	69	10.5	431 1 US-08-447-570-2	Sequence 2, Appl1
27	69	10.5	431 1 US-08-643-763A-17	Sequence 17, Appl1

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36	69	10.5	431 2 US-08-449-699A-2	Sequence 2, Appl1
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38	69	10.5	431 2 US-08-461-397A-17	Sequence 17, Appl1
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45	69	10.5	431 3 US-08-459-129-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-09-027-381-2
(Sequence 2, Application US/09027381
Patent No. 6075137)
GENERAL INFORMATION:
APPLICANT: CULP, JEFFREY
APPLICANT: MCNUITY, DEAN
APPLICANT: ELLIS, CATHERINE
TITLE OF INVENTION: HUMAN UROTENSIN II
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,381
FILING DATE: 20-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/072,383
FILING DATE: 09-JAN-1998
APPLICATION NUMBER: GP-70366-1P
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-027-381-2
Query Match 81.5%, Score 533.5, DB 3, Length 139;
Best Local Similarity 84.8%, Pred. No. 2,1e-55;
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PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
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PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
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PRIOR APPLICATION NUMBER: 60/088861
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254

PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2%; Score 279.5; DB 9; Length 124;
Best Local Similarity 49.6%; Pred. No. 1,4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 MDRVPECCLLFVGLNLPLSEPVYTDGEMSLQPLVEENALRALELELRRALLQTLRQTV 60
DB 1 MYKLASCLLFTGFLNPLSLPLDSREISFQLSAPHEDARLPFELELRASLQILPEML 60
QY 61 GTEKSSLSGQADPSAEFTPTRGSLRK--ALTGDSNTVLSRLAKRTKKQKHGTABECF 118
DB 61 GAERGDIILRKADSNTEFNPRGNILRKFDPSGODPNILLSHLARIRKPYKKRET-PDCF 119
QY 119 WKYCI 123

|||||
DB 120 WKYCV 124

RESULT 10
US-09-989-734-266
Sequence 266, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/087759
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PRIOR FILING DATE: 1998-06-03
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2%; Score 279.5; DB 9; Length 124;
Best Local Similarity 49.6%; Pred. No. 1.4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 MDRVPECLLFVGLNLSPVDTGEMSLQFLVEENALRALEELERRALLQTLRQTV 60
DB 1 MYKLASCLLFTGFLNLPLDSREISFQLSAPHEDATLPEELERASLLQILPEML 60
QY 61 GTEAGSLGADPSAEPTPRGSLRK--ALTGDSNVVLSSLLARTKOKRKHGTABECF 118
DB 61 GAEGDILIRKADSTNIFNPGNLRKFQDPSGDDPNILLSHLARIRKPYKKRET-PDCF 119

QY 119 WKYCI 123
DB 120 WKYCV 124
RESULT 11
US-09-997-653-266
Sequence 266, Application US/09997653
Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C38
CURRENT FILING DATE: 2001-11-15
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
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PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090696
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
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PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2%; Score 279.5; DB 9; Length 124;
Best local similarity 49.6%; Pred. No. 1,4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY I MDRVPECCLLFVGLNPLLSFPYTDIGEMSLQLPVLEENMLRALNEELERTALLQTLQRTV 60
I :: ||||| ||||| I :: I :: || ||||| :||| I ::
DB 1 MYKLASCCLEFTGLNPLLSPLDSREISFQLSAPHEARLPPEELERASLQILEMIL 60
QY 6I GTEAEGSLGQADPSAEPTRGSLRK--ALTGDSNTVLSRLARTKORKKHGTAPECF 118
I I I ::||| ||||| :||| I ::||| I I I ::|||
DB 6I GAERGDILRRADSSNTIFNPRGNLRKRFQDSGODPNILLSHLRLAKRYKKKRET-PDCF 119

Tue Mar 11 10:10:21 2003

us-09-831-907a-30.rapb

OY 119 WKYCI 123
Db 120 WKYCV 124

RESULT 12

US-09-993-667-266
Sequence 266, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaud, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paonli, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PicA
CURRENT APPLICATION NUMBER: US/09/993,667
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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PRIOR FILING DATE: 1997-11-13
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

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Query Match      44.2%, Score 279.5; DB 9; Length 124;
Best Local Similarity 49.6%; Pred: No. 1.4e-22;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2.

OY 1 MDWVFCCLLFFGLNPLPLSFVPTDNGEMLDPLVEENALPALLEETALLQTLRQTV 60
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DB 1 MKLLSCCLLFFGLNPLPLSLPDLDSRELSFQDSAPNHEARLPLRELEASCLLPPEML 60
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 61 GTVEAGSLQADAPASATPTTPGSLRK--ALTQDSTNTVLSRLLRKRRKQKHGTPEEF 118
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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Db	61	GAERGDILRKADSTNIENPRGNLRKFDGSGDDPNILSLHLARIWKPKKKRRT	-PDCE	119
QY	119	WKYCI	123	
		:		
Db	120	WKYCV	124	

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1 RESULT 13
2 US-09-990-438-266
3 Sequence 266, Application US/09990438
4 Publication No. US2003002754AI
5
6 GENERAL INFORMATION:
7 APPLICANT: Ashkenazi, Avi J.
8 APPLICANT: Baker, Kevin P.
9 APPLICANT: Bolstein, David
10 APPLICANT: Desnoyers, Luc
11 APPLICANT: Eaton, Dan L.
12 APPLICANT: Ferrara, Napoleone
13 APPLICANT: Fong, Sherman
14 APPLICANT: Gerber, Hanspeter
15 APPLICANT: Geritsen, Mary E.
16 APPLICANT: Goddard, Audrey
17 APPLICANT: Godowski, Paul J
18 APPLICANT: Grimaldi, J. Christopher
19 APPLICANT: Gurney, Austin L.
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21 APPLICANT: Napier, Mary A.
22 APPLICANT: Pan, James
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24 APPLICANT: Roy, Margaret Ann
25 APPLICANT: Stewart, Timothy A.
26 APPLICANT: Tumas, Daniel
27 APPLICANT: Watanabe, Colin K.
28 APPLICANT: Williams, P. Mickey
29 APPLICANT: Wood, William I.
30 APPLICANT: Zhang, Zhenli
31 APPLICANT:
32
33 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
34 TITLE OF INVENTION: Acids Encoding the Same
35 FILE REFERENCE: P2730PIC3
36 CURRENT APPLICATION NUMBER: US/09/990.438
37 CURRENT FILING DATE: 2001-11-14
38 PRIOR APPLICATION NUMBER: 60/049787
39 PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 44.2%; Score 279.5; DB 9; Length 124;
Best Local Similarity 49.6%; Pred. No. 1.4e-22;

Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 MDRVPFCCLEFVGLINPLSPYDTGEMSLQPLVEENALRALEELERFALLQTLROT 60
DB 1 MYKLASCCLEFVGLINPLSPYDTGEMSLQPLVEENALRALEELERFALLQTLROT 60
QY 61 GTEAEGSLGQADPSAETPTPGSLRK--ALTGDSNTVLSRLARTRKORRKHGTAPCECF 118

Db 61 GAERGIDLRKADSTNIFNRCNLRRFODFSGODPNILLSHLLARIMWKPKRRET-PDCE 119
Oy 119 WKYCI 123
Db 120 WKYCV 124

RESULT 14
US-09-990-562-266
Sequence 266, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhan, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C18
CURRENT APPLICATION NUMBER: US/09/990,562
CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
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PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match

Best Local Similarity 44.2%; Score 279.5; DB 9; Length 124;
Matches 62; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 MDRVPECLFVGLNPLSPPTDTCGMSLQPVLEENLRALRELEERFALLQOTLRQTV 60
DB 1 MYLASCCLFTFTLPLSLPLDSREISFOLSPHEDARLTPEELERASLLQILPEML 60

QY 61 GREAGSLGQADPSAETPPRGLRK--ALTGDSMTVLRLARTRKOROGTAPECF 118
DB 61 GAERDILRKADSTTNFENRGNLRKRFODFSGODPMLLSHLARLWKPKKRET-PDCE 119
QY 119 WKYCI 123
DB 120 WKYCV 124
RESULT 15
US-09-997-428-266
Sequence 266, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C44
CURRENT APPLICATION NUMBER: US/09/997,428
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04

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35	PRIOR APPLICATION NUMBER: 60/088826
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37	PRIOR APPLICATION NUMBER: 60/088858
38	PRIOR FILING DATE: 1998-06-11
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41	PRIOR APPLICATION NUMBER: 60/088876
42	PRIOR FILING DATE: 1998-06-11
43	PRIOR APPLICATION NUMBER: 60/089105
44	PRIOR FILING DATE: 1998-06-12
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72	PRIOR FILING DATE: 1998-06-19
73	PRIOR APPLICATION NUMBER: 60/089952

1	PRIOR FILING DATE: 1998-06-19
2	PRIOR APPLICATION NUMBER: 60/090246
3	PRIOR FILING DATE: 1998-06-22
4	PRIOR APPLICATION NUMBER: 60/090252
5	PRIOR FILING DATE: 1998-06-22
6	PRIOR APPLICATION NUMBER: 60/090254
7	PRIOR FILING DATE: 1998-06-22
8	PRIOR APPLICATION NUMBER: 60/090349
9	PRIOR FILING DATE: 1998-06-23
10	PRIOR APPLICATION NUMBER: 60/090355
11	PRIOR FILING DATE: 1998-06-23
12	PRIOR APPLICATION NUMBER: 60/090429
13	PRIOR FILING DATE: 1998-06-24
14	PRIOR APPLICATION NUMBER: 60/090431
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23	PRIOR FILING DATE: 1998-06-24
24	PRIOR APPLICATION NUMBER: 60/090535
25	PRIOR FILING DATE: 1998-06-24
26	PRIOR APPLICATION NUMBER: 60/090540
27	PRIOR FILING DATE: 1998-06-24
28	PRIOR APPLICATION NUMBER: 60/090542
29	PRIOR FILING DATE: 1998-06-24
30	PRIOR APPLICATION NUMBER: 60/090557
31	PRIOR FILING DATE: 1998-06-24
32	PRIOR APPLICATION NUMBER: 60/090676
33	PRIOR FILING DATE: 1998-06-25
34	PRIOR APPLICATION NUMBER: 60/090678
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36	PRIOR APPLICATION NUMBER: 60/090690
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56	PRIOR APPLICATION NUMBER: 60/091626
57	PRIOR FILING DATE: 1998-07-02
58	PRIOR APPLICATION NUMBER: 60/091633
59	PRIOR FILING DATE: 1998-07-02
60	PRIOR APPLICATION NUMBER: 60/091978
61	PRIOR FILING DATE: 1998-07-07
62	PRIOR APPLICATION NUMBER: 60/091982
63	PRIOR FILING DATE: 1998-07-07
64	PRIOR APPLICATION NUMBER: 60/092182
65	PRIOR FILING DATE: 1998-07-09

Query Match	44.28;	Score	279.5;	DB	9;	Length	124;
Best Local Similarity	49.68;	Pred. No.	1.4e-22;				

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QY      1 MDRVPECCLLFVGLLNPPLTSFPVDTGEMSIQLPVLEENALRALLEEELTALLQTLLRQTV    600
        | : | | | | | | | | : : | : | | | | | | | | : : | : | : | : | : | :
Db      1 MYKLASCCLLPFGFLNPLSLPLADSRKISITQLSAPHPEDARLTPPEELERKSLLQILPEML    600
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Tue Mar 11 10:10:21 2003

us-09-831-907a-30.rapb

Page 23

QY 61 GTEAGSGGADPSAETPTPGSLRK--ALTGDSDNTVLSRLARTKOROKHGTAPECE 118
DB 61 GAERDILRRKADSSTNIINPRGNLRKFODESGDPNILLSHLARLTKPKKKNET-PDCC 119
QY 119 WKYCI 123 .
DB 120 WKYCV 124

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Job time : 9.64054 secs

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OV 14 LNPLJSE-----PVTDGEMSI OF B-VI EGVARDV ENR DEEYVVO-----

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Db      2 MCNLLSFVLLSCTHLVAHPVDTADMTYSGPDSVEAGVGSPDDFAVSLDLNDLQRA 61
QY      60 VGTAEAGSLGQADPSAETPTPRGSLRKALTGODSNTVLSRLARTKQKQKHGAPECFW 119
Db      62 AVVEYSPLSLSENKIVPGQIPKEALRELLLEKPYRLIPPSGLMGSRQFRKRGGADCFW 121
QY      120 KIC1 123
Db      122 KYCV 125

RESULT 3
AG1627
single-stranded-DNA-specific exonuclease (RecJ) homolog 1ln1560 [imported] - Listeria in
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1627
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fshih, H.
; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1627
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-783 <GLA>
A:Cross-references: GB:AL59022; PIDN:CAC96791.1; PID:916414047; GSPDB:GN00178
A:Experimental source: strain C1p11262
C:Genetics:
A:Gene: 1ln1560

Query Match      13.5%; Score 85.5; DB 2; Length 783;
Best Local Similarity 31.9%; Pred. No. 2.9;
Matches 37; Conservative 16; Mismatches 36; Indels 27; Gaps 6;

QY      9 LTFVGLNPLSPVYTDGEMSLQLPV--LEENALRALELEERTALL--QTLRQTVG-- 61
Db      221 LVAVGTVDLV--LTDENRLVQLGRLQRLRENANGLAVLAKKASKLEETEETIGFG 278

QY      62 ----TEAGSLGQADPSAE--TTPRGSLRKALTGODSNTVLSRLARTKQKQK 110
Db      279 LARLNAVGRIGPADPADLLTEDEPFLAEELIDAN-----KERKQ 323

RESULT 4
S10706
urotensin II precursor - European flounder (fragments)
C:Species: platichthys flesus (European flounder)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 21-Nov-1998
C:Accession: S10706
R:Conlon, J.M.; Arnold-Reed, D.; Balmert, R.J.
FEBS Lett. 266, 37-40, 1990
A:Title: Post-translational processing of prepro-urotensin II.
A:Reference number: S10706; MUID:90306357; PMID:2365069
A:Accession: S10706
A:Molecule type: protein
A:Residues: 1-83 <CON>
A:Experimental source: urophysse
C:Superfamily: urotensin II
C:Keywords: neuropeptide; osmoregulation
F:1-71/Product: urotensin II #status experimental <MAT>
F:72-83/Domain: carboxyl-terminal propeptide #status experimental <PRO>
F:77-82/Disulfide Bonds: #status predicted

Query Match      13.4%; Score 85; DB 2; Length 83;
Best Local Similarity 27.5%; Pred. No. 0.23;
Matches 30; Conservative 12; Mismatches 33; Indels 34; Gaps 5;

QY      22 PVTDTGEMSLQLPV--LEENALRALELEERTALLQTLRQTVGTEAGSLGQADPSAETPTP 80

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Db      2 PITSEAMPPPGPSLBERGSLDDL-----SLSEGN-----YPPQ 38
QY      81 RG-----SLRKALTGODSNTVLSRLARTKQKQKHGAPECFWKYC1 123
Db      39 RGAGLRATLEVLLEKQSLNPFPSRVG-----IRKQAGTTECFWKYCV 83

RESULT 5
G70767
probable helicase hely - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: G70767
R:Colo, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrett, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70767
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-906 <COL>
A:Cross-references: GB:273966; GB:AL123456; NID:93261577; PIDN:CAA98204.1; PID:e24701
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: hely

Query Match      12.9%; Score 81.5; DB 2; Length 906;
Best Local Similarity 32.8%; Pred. No. 8.5;
Matches 39; Conservative 9; Mismatches 48; Indels 23; Gaps 7;

QY      11 FVGLL--NPLLSFPVTD--TGEMSLQLPVLEENALRALELEERTALLQTLR----- 57
Db      711 FVGLLTERFPGPATDPVYTDGRLARITYESDULVAECL-RFGAMGGLPAELAGV 769

QY      58 QTVGTEAGSLGQADP-SAETPTPRGSLRKALTGODSNTVLSRLARTKQKQKHGTAP 115
Db      770 SAVVETRGCGDQGAAPGADVPTPR--LRQAL-----TQTSRLSTYLRADQAHRTIP 820

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RESULT 6
AE1265
single-stranded-DNA-specific exonuclease (RecJ) homolog 1mo1525 [imported] - Listeria
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1265
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fshih,
; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1265
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-783 <GLA>
A:Cross-references: GB:IN003210; PIDN:CAC99603.1; PID:916410954; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: 1mo1525

Query Match      12.7%; Score 80.5; DB 2; Length 783;
Best Local Similarity 31.0%; Pred. No. 8.9;
Matches 36; Conservative 17; Mismatches 36; Indels 27; Gaps 6;

QY      9 LTFVGLNPLSPVYTDGEMSLQLPV--LEENALRALELEERTALL--QTLRQTVG-- 61
Db      221 LVAVGTVDLV--LTDENRLVQLGRLQRLRESANGLAVLAKKASKLEETEETIGFG 278

```


ATP-dependent helicase XF0882 (imported) - *Xylella fastidiosa* (strain 9a5c)

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AH3009
 A>Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-2399 <KUR>
 A:Cross-References: GB:AE008689; PIDN:AAL44494.1; PID:917742101; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: mtad
 A:Map position: linear chromosome

Query Match 11.7%; Score 74; DB 2; Length 2399;
 Best Local Similarity 27.4%; Pred. No. 1.4e+02;
 Matches 37; Conservative 9; Mismatches 43; Indels 46; Gaps 7;

QY 12 VGLNP--LLSPVYDTGMSLQPLVLEENALR-ALAELEERTALLQT-----55
 DB 1927 LGRLPEGLLEF---LGRDFQVKV---NGFRLEGELE-TALLQENNVAAVVTWQ 1978
 QY 56 -----LQQTGTEAGSLGQADPSAETPTPRGSLRKALTGQDSNTV 96
 DB 1979 PPALAIYVPTKGLICKLEAKGRSGNGGLGDAGRYVDPDPLGHEATROSHRRF 2038
 QY 97 LSRLARTRKQKOH 111
 DB 2039 LN---APTELQKIGH 2050

RESULT 15

AD0700

probable two-component sensor kinase ssra [imported] - *Salmonella enterica* subsp. enteri
 C:Species: *Salmonella enterica* subsp. enterica serovar typh
 A:Note: this species has also been called *Salmonella typhi*
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AD0700
 R:Parikh, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AD0700
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-920 <PAR>
 A:Cross-References: GB:AL51382; PIDN:CAD01973.1; PID:916502815; GSPDB:GN00176
 C:Genetics:
 A:Gene: ssra

Query Match

Best Local Similarity 11.5%; Score 73; DB 2; Length 920;
 Matches 37; Conservative 15; Mismatches 54; Indels 30; Gaps 6;

QY 6 FCCLFVGLNPLSF---PVTDTGMSLQPLVLEENALRALEELERT-----LLQTL 56
 DB 311 FCWLLHRSIAKPLMFVDIINTATAPLSTRPA-----QRLDELDSIAGAFNQLDLTL 364
 QY 57 R-----QTVGTEAGSLGQADPSAETPTPRGSLRKALTGQDSNTVLS-----RLART 104
 DB 365 QVQYDNLENKVAERTQALNEAKKRAEQANKRSIHLYISHLRTPMNGVLCATIELQTT 424
 QY 105 RKQKQHG---TAPEC 117
 DB 425 PLNIEQOGLADTARNC 440

Search completed: March 10, 2003, 17:47:27
 Job time : 15.2973 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:26:37 ; Search time 6.98108 Seconds

(without alignments)
730.773 Million cell updates/sec

Title: US-09-831-907A-30

Perfect score: 633
Sequence: 1 MDRVPCCLLVGLNPLLS.....TRKOROKHGTAPCECFWKYCI 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	633	100.0	123	1. UR2_RAT	Q9qzq4 rattus norv
2	541	85.5	123	1. UR2_MOUSE	Q9qzq3 mus musculu
3	282.5	44.6	124	1. UR2_HUMAN	O9q399 homo sapien
4	128	20.2	127	1. UR2_RANR1	P33715 rana ridibu
5	107	16.9	125	1. UR2G_CYPCA	P06580 cyprinus ca
6	104	16.4	125	1. UR2A_CYPCA	P04560 cyprinus ca
7	85	13.4	83	1. UR2_PLAF6	P21857 platichthys
8	81.5	12.9	906	1. HELY_MYCMU	Q10701 mycobacteri
9	76	12.0	468	1. SYE_THERH	P27000 thermus the
10	75	11.8	523	1. E2BD_RABIT	P41111 oryctolagus
11	74	11.7	1076	1. NDPI_YEAST	P03129 rickettsia
12	73	11.5	1374	1. RPOB_RICPR	O62271 rickettsia
13	72.5	11.5	404	1. EAD_EBV	P03129 rickettsia
14	72.5	11.5	926	1. POBL_YEAST	Q01454 saccharomyc
15	72	11.4	920	1. HELY_MYCLE	Q9zbd8 mycobacteri
16	72	11.4	1581	1. LMG3_MOUSE	Q9zbd8 mus musculu
17	71.5	11.3	311	1. UCP3_CANFA	O9z319 canis fami
18	71.5	11.3	409	1. ODO2_HAEIN	P45302 haemophilus
19	71	11.2	1373	1. RPOB_RICCN	Q9zbd8 rickettsia
20	71	11.2	1373	1. RPOB_RICCN	Q9zbd8 rickettsia
21	70.5	11.1	207	1. FM2_BORPE	O77792 bos taurus
22	70.5	11.1	311	1. UCP3_BOVIN	O9z319 canis fami
23	70.5	11.1	523	1. E2BD_HUMAN	Q9zbd8 mus musculu
24	70	11.1	337	1. NAFL_MOUSE	Q9zbd8 mus musculu
25	69.5	11.0	337	1. G3PE_MAIZE	Q43247 zea mays (m
26	69.5	11.0	381	1. AMPC_ENTCL	P05364 enterobacte
27	68.5	10.8	632	1. PARE_HAEIN	P43703 haemophilus
28	68.5	10.8	5327	1. ACPT_MOUSE	Q9zbd8 mus musculu
29	68	10.7	842	1. P2CG_MOUSE	O61074 mus musculu
30	68	10.7	842	1. MK07_HUMAN	O50314 homo sapien
31	68	10.7	1279	1. BCHH_CHLVI	O50314 chloobidum
32	67.5	10.7	318	1. ANK5_RAT	P14668 rattus norv
33	67.5	10.7	357	1. NDPI_CHICK	P79765 gallus gall

34	67.5	10.7	374	1. ERGL_MOUSE	O8vcd3 mus musculu
35	67.5	10.7	630	1. PARE_SALTY	P31598 salmonella
36	67	10.6	269	1. TRPA_BACST	P19867 bacillus st
37	67	10.6	354	1. DCUP_SYN7	P16891 synechococc
38	67	10.6	604	1. VEI_BPV2	P11298 bovine papl
39	67	10.6	878	1. MSH4_YEAST	P40865 saccharomyc
40	67	10.6	1206	1. FM14_MOUSE	O03859 mus musculu
41	67	10.6	1363	1. RPOB_HAEIN	P43738 haemophilus
42	66.5	10.5	361	1. RECA_BRUME	O8yhl0 brucella me
43	66.5	10.5	673	1. FYUA_YEREN	P46360 yersinia en
44	66.5	10.5	673	1. FYUA_YERPE	P46359 yersinia pe
45	66.5	10.5	886	1. APCE_PORPU	P51263 porphyra pu

ALIGNMENTS

RESULT 1

UR2_RAT STANDARD: PRT: 123 AA.

AC Q9QZQ4; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II precursor (U-II) (UII).
GN UTS2.

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=spinal cord;
RX MEDLINE=99416011; PubMed=10486557;
RA Coulouarn Y., Jegou S., Tostivint H., Vaudry H., Lihmann I.;
RT "Cloning, sequence analysis and tissue distribution of the mouse and
RT rat urotensin II precursors.";
RL FEBS Lett. 457:28-32(1999).
CC -!- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC -!- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

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CC or send an email to license@sib-sib.ch).

DR EMBL; AF172174; AAD55766.1; -
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin_II.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PROPEP 21 104
FT PEPTIDE 110 123
FT DISULFID 117 122
FT SEQUENCE 123 AA; 13614 MW; EFH18EE124AF1BA CRC64;

Query Match 100.0%; Score 633; DB 1; Length 123;
Best Local Similarity 100.0%; Pred. No. 6.4e-54;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MDRVPCCLLVGLNPLSPVDTGEMSLQDPELNARALELERTALLQTLQTV	60
DB	1	MDRVPCCLLVGLNPLSPVDTGEMSLQDPELNARALELERTALLQTLQTV	60
QY	61	GTEAEGSLGADPSAETPTPGSLRKALTGDSNTVLSRLIARRKOROKHGTAPCECFWK	120
DB	61	GTEAEGSLGADPSAETPTPGSLRKALTGDSNTVLSRLIARRKOROKHGTAPCECFWK	120

QY 121 YC1 123
DB 121 YC1 123

RESULT 2
UR2_MOUSE STANDARD: PRT: 123 AA.

AC Q9QZ03;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urotensin II precursor (U-II) (UII).
GN UTS2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=99416011; PubMed=10486557;
RA Coulouarn Y., Jegou S., Tostivint H., Vaudry H., Lihmann I.;
RT "Cloning, sequence analysis and tissue distribution of the mouse and
rat urotensin II precursors."
RL FEBS Lett. 457:28-32(1999).
CC -1- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC. PREDOMINANTLY EXPRESSED IN
MOTONEURONS OF THE BRAINSTEM AND SPINAL CORD.
CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

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CC -----
DR EMBL: AF172175; AAD55767.1; -
DR MGD: MGI:1346329; Uts2.
DR InterPro: IPR001483; Urotensin-II.
DR Pfam: PF02083; Urotensin-II: 1.
DR PROSITE: PS00984; UROTENSIN_II: 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 104 POTENTIAL.
FT PEPTIDE 110 123 UROTENSIN II.
FT DISULFID 117 122 BY SIMILARITY.
SQ SEQUENCE 123 AA: 13625 MW: F96486195137F7F4 CRC64;

Query Match Score 541; DB 1; Length 123;
Best Local Similarity 84.6%; Pred. No. 4, 1e-45;
Matches 104; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 1 MDRVPCCLLFVGLNPLSPVTDGEMSLQPLVEENALRALELELRTALLQTLRQTV 60
DB 1 MDRVPCCLLFVGLNPLSPVTDGERTLQPLVEEDALRALELELRTALLQTLRQTM 60
QY 61 GTEAEGSLQADPSAETPPRGSLRKALTGODSNVLSRLARTKQRQKHGTAPPCFPK 120
DB 61 GTEAEGSPGEAGPSTETPPRGSMRKAFAGONSNTVLSRLARTKQRKHGAAPPCFPK 120
QY 121 YC1 123
DB 121 YC1 123

RESULT 3
UR2_HUMAN STANDARD: PRT: 124 AA.

AC O95399; Q9UKP7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urotensin II precursor (U-II) (UII).
GN UTS2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=99080095; PubMed=9861051;
RA Coulouarn Y., Lihmann I., Jegou S., Anouar Y., Tostivint H.,
RT Beauvillain J.C., Conlon J.M., Bern H.A., Vaudry H.;
RT "Cloning of the cDNA encoding the urotensin II precursor in frog and
human reveals intense expression of the urotensin II gene in
motoneurons of the spinal cord."
RL Proc. Natl. Acad. Sci. U.S.A. 95:15803-15808(1998).

CC SEQUENCE FROM N.A.
CC MEDLINE=99427933; PubMed=10499587;
CC Ames R.S., Sarau H.M., Chambers J.K., Willette R.N., Aiyar N.V.,
CC Romanic A.M., Loudon C.S., Foley J.J., Sauermelch C.F., Coetney R.W.,
CC Ao Z., Disa J., Holmes S.D., Stadel J.M., Martin J.D., Liu W.-S.,
CC Glover G.T., Wilson S., McNulty D.E., Ellis C.E., Elshourbagy N.A.,
CC Shabon U., Trill J.J., Hay D.W.P., Ohlstein E.H., Bergsma D.J.,
CC Douglas S.A.;
CC "Human urotensin-II is a potent vasoconstrictor and agonist for the
orphan receptor GPR14."
CC Nature 401:282-286(1999).
CC [3]
CC SEQUENCE FROM N.A.
CC Pearce A.;
CC Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

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CC -----
DR EMBL: AF104118; AAD13070.1; -
DR EMBL: AF140630; AAD5577.1; -
DR EMBL: Z98884; CAB63148.1; -
DR Genew: HGNC:12636; UTS2.
DR MIM: 604097; -
DR InterPro: IPR001483; Urotensin-II.
DR Pfam: PF02083; Urotensin-II: 1.
DR PROSITE: PS00984; UROTENSIN_II: 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT PROPEP 21 110 UROTENSIN II.
FT PEPTIDE 114 124 BY SIMILARITY.
FT DISULFID 118 123 MYKLSCLFGLFGLNPL -> METNVEHLMLCVTSARTH
FT CONFLICT 1 19 KTSLSLGFHNSYP (IN REF. 2).
FT CONFLICT 24 27 LDSR -> IHDLL (IN REF. 2).
SQ SEQUENCE 124 AA: 14295 MW: C7A5FC7EFED0D312 CRC64;

Query Match Score 282.5; DB 1; Length 124;
Best Local Similarity 49.6%; Pred. No. 2, 3e-20;
Matches 62; Conservative 17; Mismatches 43; Indels 3; Gaps 2;

QY 1 MDRVPCCLLFVGLNPLSPVTDGEMSLQPLVEENALRALELELRTALLQTLRQTV 60
DB 1 MDRVPCCLLFVGLNPLSPVTDGEMSLQPLVEENALRALELELRTALLQTLRQTV 60

Db 1 MYLASCCLLFGFLNPLSLPLDLSRELSFQLSAPHEADRLPEELERALLQILPEML 60
 QY 61 GTEAGSLGADPSAETPTPRGSLRK--ALTGDSMTVLSRLARRKOROKGTPECF 118
 Db 61 GAEGRDILKKAUSSTNIENRGNLRKFOFSGDPNILLSHLARIMKPKRRET-PDGF 119
 QY 119 MKYCI 123
 Db 120 MKYCV 124

RESULT 4
 UR2_RANRI
 ID UR2_RANRI STANDARD: PRT: 127 AA.
 AC P33715: QPSPX6;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Urotensin II precursor (U-II) (UII).
 GN UT52.
 OS Rana ridibunda (laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxId=8406;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99080095; PubMed=9861051;
 RA Couloaren Y., Lihmann I., Jegou S., Anouar Y., Testavint H.,
 RA Beauvillain J.C., Conlon J.M., Bern H.A., Vaudry H.;
 RT "Cloning of the cDNA encoding the urotensin II precursor in frog and
 RT human reveals intense expression of the urotensin II gene in
 RT motoneurons of the spinal cord.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:15803-15808(1998).
 RN [2]
 RP SEQUENCE OF 115-127.
 RC TISSUE=Brain;
 RX MEDLINE=93075134; PubMed=1445302;
 RA Conlon J.M., O'Harte F., Smith D.D., Tonon M.-C., Vaudry H.;
 RT "Isolation and primary structure of urotensin II from the brain of a
 RT tetrapod, the frog Rana ridibunda.";
 RL Biochem. Biophys. Res. Commun. 188:578-583(1992).
 CC -1- FUNCTION: INVOLVED IN SMOOTH MUSCLE STIMULATING AND ION
 CC MOBILIZING ACTIVITIES. IT HAS A SUGGESTED ROLE AS A
 CC CORTICOTROPIN-RELEASING FACTOR.
 CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM. SPINAL CORD.
 CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF104117; AADI3069.1; -
 DR PIR: P00445; P00445.
 DR InterPro: IPR001483; Urotensin_II.
 DR Pfam: PF02083; Urotensin_II.1
 DR PROSITE: PS00984; UROSENSIN_II.1.
 KW Hormone; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 16
 FT PROPEP 17 111
 FT PEPTIDE 115 127 UROSENSIN II.
 FT DISULFID 121 126
 SO SEQUENCE 127 AA; 14732 MW; FC26BC90E00C082E CRC64;

Query Match 20.2%; Score 128; DB 1; Length 127;
 Best Local Similarity 29.6%; Pred. No. 1.5e-05;
 Matches 40; Conservative 20; Mismatches 55; Indels 20; Gaps 5;

1 MDRVPCCLLFVGLNPLSLFP--VTDTGENSIQLPYLEENALRALEELERTALLQTLRQ 58

Db 1 MSKLFCCCLLAGSFCFSFRSLPIIVPSKGLRLSESALDGDGLKSWD--DETLNPLPM 58
 QY 59 TVGTAEAGSLGADPSAETPTPRGSLRKALITGDSN-----TVLSRLARTKQ-R 108
 Db 59 FVDKEARD-----AEDLFSKEGFGIDAVNMMDKEELFDKHPRIILSLRQSKDRKQK 112
 QY 109 KQHTAPECFWKYCI 123
 Db 113 KRAGNLSECFWKYCV 127

RESULT 5
 UR2G_CYPCA
 ID UR2G_CYPCA STANDARD: PRT: 125 AA.
 AC P06580;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE UII gamma precursor (contains: Urophysin gamma; Urotensin II-gamma).
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxId=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86307061; PubMed=2427672;
 RA Ohsako S., Ishida I., Ichikawa T., Deguchi T.;
 RT "Cloning and sequence analysis of cDNAs encoding precursors of
 RT urotensin II-alpha and -gamma.";
 RL J. Neurosci. 6:2730-2735(1986).
 RN [2]
 RP SEQUENCE OF 114-125.
 RA Munekata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
 RL (In) Rich D.H., Gross E. (eds.);
 RL Proceedings of the 7th American peptide symposium, pp.69-72.
 CC Pierce Chemical Co., Rockford IL. (1981).
 CC -1- FUNCTION: UROSENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
 CC PRECURSOR MAY BE A UROSENSIN BINDING PROTEIN, UROPHYSIN.
 CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
 CC -----
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 CC -----
 DR EMBL: M14088; AAA49216.1; -
 DR InterPro: IPR001483; Urotensin_II.
 DR Pfam: PF02083; Urotensin_II.1
 DR PROSITE: PS00984; UROSENSIN_II.1.
 KW Hormone; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 106 UROPHYSIN GAMMA (POTENTIAL).
 FT PEPTIDE 114 125 UROSENSIN II-GAMMA.
 FT DISULFID 119 124
 SO SEQUENCE 125 AA; 13866 MW; E1587DCFC8CB674D CRC64;

Query Match 16.9%; Score 107; DB 1; Length 125;
 Best Local Similarity 27.1%; Pred. No. 0.0015;
 Matches 32; Conservative 24; Mismatches 60; Indels 2; Gaps 2;

7 CCLLFVGLNPLSLFPVTDGKSLQLP-VLEENALRALEELERTALLQTLRQVTGEAE 65
 Db 9 CSVLLS-CSHLNHPVTDADMTYSGPDSEAGVNPDDFSVDNENHLQRAAVAGYS 67
 QY 66 GSILGADPSAETPTPRGSLRKALITGDSNIVLSRLARTKQKQHTAPECFWKYCI 123

Db 68 PLFSGENIKVPGQIPKPEALRELLLEKPYRLIPRGLWSGHROFRRKRGAGDCEWKC1 125

RESULT 6
UR2A_CYPCA STANDARD; PRT; 125 AA.

AC P04560:
DE 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Uti alpha precursor [contains: Urophysin alpha: urotensin II-alpha].
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprini.
NCBI_Taxid=7962;

RP SEQUENCE FROM N.A.
RX MEDLINE=66307061; PubMed=2427672;
RA Ohsaka S., Ishida I., Ichikawa T., Deguchi T.;
RT "Cloning and sequence analysis of cDNAs encoding precursors of
urotensin II-alpha and -gamma."
RJ J. Neurosci. 6:2730-2735(1986).

RL J. Neurosci. 6:2730-2735(1986).

RP SEQUENCE OF 114-125.
RA Murekata F., Ohkaki T., Ichikawa T., McMaster D., Lederis K.;
RL (in) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th American peptide symposium, pp.69-72,
Pierce Chemical Co., Rockford IL. (1981).

CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
PRECURSOR MAY BE A UROTENSIN BINDING PROTEIN, UROPHYSIN.

CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

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CC EMBL: M14084; AAA9215.1;
DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II.1.
DR PROSITE: PS00984; UROTENSIN_II.1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT CHAIN 22 106 UROPHYSIN ALPHA (POTENTIAL).
FT PEPTIDE 114 125 UROTENSIN II-ALPHA.
FT DISULFD 119 124
SQ SEQUENCE 125 AA; 13840 MW; 1F6BF66CA6B3A5AF CRC64;

Query Match 15.4%; Score 104; DB 1; Length 125;
Best Local Similarity 25.8%; Pred. No. 0.0078;
Matches 32; Conservative 23; Mismatches 55; Indels 14; Gaps 2;

QY 14 LNLPLSF-----PVTDTGMSLQPV-LEENALALELEERTALQTLQRT 59
DB 2 MCNLLISFVLLSCTHLVAHPYTDADMTYSGPSVPEAGVSPDPFVSLNDLQRA 61

QY 60 VGTAEAGSLGADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKQKHGTAFECFW 119
DB 62 AVEYSPILSRKIKVPGQIPKPEALRELLLEKPYRLIPRGLWSGHROFRRKRGAGDCEW 121

QY 120 KYCI 123
DB 122 KYCV 125

RESULT 7
UR2_PLAFA

ID UR2_PLAFA STANDARD; PRT; 83 AA.

AC P21857;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II precursor (U-II) (III) (Fragments).
OS Platycthis flesus (European flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Pleuronectidae; Platycthis.
NCBI_Taxid=8260;

RP SEQUENCE.
RC TISSUE=Urophysis;
RX MEDLINE=90306357; PubMed=2365069;
RA Conlon J.M., Arnold-Reed D.E., Balmert R.J.;
RT "Post-translational processing of prepro-urotensin II.";
RJ FEBS Lett. 266:37-40(1990).

CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
PRECURSOR MAY BE A UROTENSIN BINDING PROTEIN, UROPHYSIN.

CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.

DR PIR: S10706; S10706.
DR InterPro: IPR001483; Urotensin_II.
DR PROSITE: PS00984; UROTENSIN_II.1.
KW Hormone; Cleavage on pair of basic residues.
FT NON_TER 1 1
FT PEPTIDE 1 48 UROPHYSIN (POTENTIAL).
FT NON_CONS 48 49
FT NON_CONS 71 72
FT PEPTIDE 72 83 UROTENSIN II.
FT DISULFD 77 82
SQ SEQUENCE 83 AA; 9292 MW; 6DD057577E6DF703 CRC64;

Query Match 13.4%; Score 85; DB 1; Length 83;
Best Local Similarity 27.5%; Pred. No. 0.11;
Matches 30; Conservative 12; Mismatches 33; Indels 34; Gaps 5;

QY 22 PVTDTGMSLQPV-LEENALALELEERTALQTLQRTVGTAEAGSLGADPSAETPTP 80
DB 2 PTTESAEMPPYPASLEEGVSGSLDLD-----SLSEQN-----YPPQ 38

QY 81 RG-----SLRKALTGDSNTVLSRLARTRKQKHGTAFECFWKCYC1 123
DB 39 KAGLRATLEVLLEKQSLNLFNSVFG---IRRGFAGTTCDFWKCVC 83

RESULT 8
HELX_MYCTU STANDARD; PRT; 906 AA.

ID HELX_MYCTU
AC Q10701;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable helicase helv (EC 3.6.1.-).
GN HELX OR RVZ092C OR MT2153 OR MTCY49.32C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
NCBI_Taxid=1773;

RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G. ;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence."
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDL 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W. ;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains." ;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE HELICASE FAMILY. SR12 SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: Z73866; CAA98204.1; -
 DR EMBL: AE007064; AAK46434.1; -
 DR TIGR: MT2153; -
 DR Tuberculist: RV2092c; -
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00270; DEAD; 1.
 DR Pfam: PF00271; helicase_C; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HelicC; 1.
 KW Hydrolyase; Helicase; ATP-binding; Complete proteome.
 FT NP_BIND 39 46 ATP (POTENTIAL).
 FT SITE 132 135 DEH BOX.
 SQ SEQUENCE 906 AA; 99606 MW; CC0A34A9495AE568 CRC64;
 Query Match 12.9%; Score 81.5; DB 1; Length 906;
 Best Local Similarity 32.8%; Pred. No. 4.2;
 Matches 39; Conservative 9; Mismatches 48; Indels 23; Gaps 7;
 QY 11 FVGLL--NPILSPVPTD---TGEMSLQPVLEENALRLLEELRTALLQITR----- 57
 Db 711 FVGLITEREFIDGPATPVVTDGRLRLARISESDLVAECL-RTGMEGLKPAELAGV 769
 QY 58 QTVGTEAGSLGQADP-SAEPTPRGSLRKALTGODSNTVLSRLLRKRKRKHGTAP 115
 Db 770 SAVVYERFGDGCGAPFGADVPTPR--LRQL-----TQTSRLSTLRLADEQAHRITP 820
 RESULT 9
 SYE_THETH
 ID SYE_THETH STANDARD; PRT; 468 AA.
 AC P27000;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GLUTS).
 GN GLTX.
 OS Thermus thermophilus.
 OC Bacteria; Thermus/Delinoococcus group; Deinococci; Thermales;
 OC Thermaceae; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB8 / ATCC 27634;
 RA MEDLINE=92174899; PubMed=1541262;
 RA Nureki O., Suzuki K., Hara-Yokoyama M., Kohno T., Matsuzawa H.,
 RA Ohta T., Shimizu T., Morikawa K., Miyazawa T., Yokoyama S. ;

RT "Glutamyl-tRNA synthetase from Thermus thermophilus HB8. Molecular
 RT cloning of the gltx gene and crystallization of the overproduced
 RT protein." ;
 RL Eur. J. Biochem. 204:465-472(1992).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RC STRAIN=HB8 / ATCC 27634;
 RA MEDLINE=95215840; PubMed=7701318;
 RA Nureki O., Vassylyev D.G., Katayanagi K., Shimizu T., Sekine S.-I.,
 RA Kigawa T., Miyazawa T., Yokoyama S., Morikawa K. ;
 RT "Architectures of class-defining and specific domains of glutamyl-tRNA
 RT synthetase." ;
 RL Science 267:1958-1965(1995).
 CC -I- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamyl-tRNA(Glu).
 CC -I- SUBUNIT: MONOMER.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X64557; CAA45854.1; -
 DR PIR: S21172; S21172.
 DR PIR: S21236; S21236.
 DR PDB: 1GLN; 15-OCT-95.
 DR InterPro: IPR004527; Gltx_bact.
 DR InterPro: IPR000924; Glu_tRNA-synt_1c.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00749; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTHGLU.
 DR TIGRFAMS: TIGR00464; gltx_bact; 1.
 DR PROSITE: PS00178; AA-TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW 3D-structure.
 FT SITE 8 18 "HIGH" REGION.
 FT SITE 243 247 "KMSKS" REGION.
 FT BINDING 246 246 ATP.
 SQ SEQUENCE 468 AA; 53901 MW; BD8A141031BE06ED CRC64;
 Query Match 12.0%; Score 76; DB 1; Length 468;
 Best Local Similarity 36.8%; Pred. No. 6.5;
 Matches 35; Conservative 9; Mismatches 31; Indels 20; Gaps 6;
 QY 21 FPIVDTGEMSLQ--LPVEE--NMLRALEELERRALLQTLQVGTGTEAG--SLGQ-ADP 73
 Db 377 YPVEKAQRKLEBGLPLKLELPRLRAOEWEALALRLR--GFAEKGVKLGQVAOP 433
 QY 74 SAEPTPRGSLRKALTGODSNTVLSRLLRKRKR 108
 Db 434 -----LRAALTGSLERPGLEIALLGKR 458
 RESULT 10
 E2BD-RABIT
 ID E2BD-RABIT STANDARD; PRT; 523 AA.
 AC P41111;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Translation initiation factor eIF-2B delta subunit (eIF-2B GDP-GTP
 DE exchange factor).
 GN EIF2B4 OR EIF2BD.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-New Zealand white; TISSUE-Liver;
RA MEDLINE-9415399; PubMed-0110836;
RA Price N.T., Francia G., Hall L., Proud C.G.;
RT "Guanine nucleotide exchange factor for eukaryotic initiation
RT factor-2. Cloning of cDNA for the delta-subunit of rabbit translation
RT Initiation factor-2B." 1217:207-210(1994).
RL Blochlin, Blodys. Acta 210(1994).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR
CC -2- BOUND GDP FOR GTP.
CC -1- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
CC DELTA AND EPSILON.
CC -1- SIMILARITY: BELONGS TO THE EIF-2B ALPHA/BETA/DELTA SUBUNITS
CC FAMILY.
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DR EMBL; X75451; CA53204.1; ALT_INIT.
DR InterPro; IPR000649; IF-2B.
DR Pfam; PF01008; IF-2B; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 523 AA; 57120 MW; 057895B1E9D25558 CRC64;

Query Match 11.8%; Score 75; DB 1; Length 523;
Best Local Similarity 32.9%; Pred. No. 9.3;
Matches 27; Conservative 9; Mismatches 36; Indels 10; Gaps 3;

QY 42 RALELEERALLQTRQVGTAEBSLGOADPSAEPPRGSLSR-KALTGDSNTVLSRL 100
DB 144 RAKQAEER-----ALKQARKGEGGPPQAPSPSTAGEAPAGSKRLTEHTQADPTLLRL 158
QY 101 LARTRKO-----RKQGTAPCEP 118
DB 159 VKSERQOVPTRKDYGSYSLF 180

RESULT 11
NUP1_YEAST
ID NUP1_YEAST STANDARD: PRT: 1076 AA.
AC P20676;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nucleoporin NUP1 (Nuclear pore protein NUP1).
GN NUP1 OR YOR098C OR YOR3182C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-90275616; PubMed-2190694;
RA Davis L.I., Fink G.R.;
RT "The NUP1 gene encodes an essential component of the yeast nuclear
RT pore complex." 1990.
RL Cell 61:965-978(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-97344368; PubMed-9200815;
RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
RA Schwaeger C., Paces V., Sander C., Ansoerge W.;
RT "DNA sequencing and analysis of 130 kb from yeast chromosome XV." 1997.
RL Ycast 13:655-672(1997).
CC -1- FUNCTION: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
CC NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLOCATION OF
CC THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Nuclear pore complex.

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CC -1- DOMAIN: APPEARS TO BE DIVIDED INTO THREE DOMAINS DEFINED BY
CC CENTRALLY LOCATED REPEATING UNITS. FUNCTIONAL N-TERMINAL OF NUP1
CC OR OF NUP2 IS REQUIRED FOR GROWTH.
CC -1- DOMAIN: CONTAINS F-X-F-G REPEATS.
CC -1- SIMILARITY: TO THE CENTRAL REPEATING UNITS OF NSP1 AND NUP2, AND
CC TO MAMMALIAN P02.
-----
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DR EMBL; M33632; AAA34822.1; -
DR EMBL; X94335; CA64020.1; -
DR EMBL; 275006; CA99295.1; -
DR PIR; A35622; A35622.
DR SGD; S0005624; NUP1.
KW Nuclear protein; Transport; Repeat.
FT DOMAIN 333 949 29 X 9 AA APPROXIMATE REPEATS.
SQ SEQUENCE 1076 AA; 113581 MW; 4AC23567D2FEB35CC CRC64;

Query Match 11.7%; Score 74; DB 1; Length 1076;
Best Local Similarity 26.6%; Pred. No. 27;
Matches 33; Conservative 21; Mismatches 48; Indels 22; Gaps 7;

QY 17 PLTSFPTVDTGMSQLDPLVEENALALELEERTALQTRQVGTAE-----GSL 68
DB 86 PLITGTENTETERPPL-LPILPQRLRLREKQVRNMRELGLQSTEFPSINSVYLGSQ 144
QY 69 GOADP-----SAETPTP--KGLRKAL---TGDSNTVLSULA-KRKQKQ-KGTAP 115
DB 145 SKSDEGSGYLCTSSNPPIKNGSCITROLAGSGEDTNGPLITKSLKNSNKRKHSQSK 204
QY 116 ECFW 119
DB 205 GTVW 208

RESULT 12
RPOB_RICPR
ID RPOB_RICPR STANDARD: PRT: 1374 AA.
AC O52271; O5RH37;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase beta chain (PC 2.7.7.6) (transcriptase
DE beta chain) (RNA polymerase beta subunit).
GN RPOB OR RPI40.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsia.
OX NCBI_TaxID=782;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-Madrid E;
RA MEDLINE-98215179; PubMed-9555894;
RA Racheh L.I., Tucker A.M., Winkler H.H., Wood D.O.;
RT "Transformation of Rickettsia prowazekii to rifampin resistance." 1998.
RL J. Bacteriol. 180:2118-2124(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-Madrid E;
RA MEDLINE-99039499; PubMed-9823893;
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sierichitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kuiland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria." 1998.
RL Nature 396:133-140(1998).
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN-Breintl;
RX MEDLINE=99437773; PubMed=10508014;
RA Drancourt M., Reault D.;
RT "Characterization of mutations in the rpoB gene in naturally
RL rifampin-resistant Rickettsia species.";
CC Antimicrob. Agents Chemother. 43:2400-2403(1999).
CC -I- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -I- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).
CC -I- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -I- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY
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CC -----
DR EMBL; AF034531; AAC38354.1; -
DR EMBL; AJ235270; CAAL4608.1; -
DR EMBL; AF076437; AAF2439.1; -
DR HSSP; O9KMU7; IHOM.
DR InterPro: IPR001572; RNA_POL_B.
DR Pfam; PF00562; RNA_POL_B.1.
DR PROSITE; PS01166; RNA_POL_BETA_1.
KW Transcription: DNA-directed RNA polymerase: Transcription:
KW Antibiotic resistance: Complete proteome.
FT VARIANT 10 10 S -> A (IN STRAIN BREINL).
FT VARIANT 15 15 H -> L (IN STRAIN BREINL).
FT VARIANT 19 19 I -> L (IN STRAIN BREINL).
FT VARIANT 96 96 D -> E (IN STRAIN BREINL).
FT VARIANT 195 195 R -> I (IN STRAIN BREINL).
FT VARIANT 216 216 K -> R (IN STRAIN BREINL).
FT VARIANT 256 256 K -> E (IN STRAIN BREINL).
FT VARIANT 273 273 D -> Y (IN STRAIN BREINL).
FT VARIANT 282 282 K -> N (IN STRAIN BREINL).
FT VARIANT 299 299 G -> S (IN STRAIN BREINL).
FT VARIANT 310 310 L -> F (IN STRAIN BREINL).
FT VARIANT 546 546 R -> K (IN RIFAMPIN RESISTANT MUTANT).
SQ SEQUENCE 1374 AA; 154582 MW; 384676DF6584DB4 CRC64;

Query Match 11.5%; Score 73; DB 1; Length 1374;
Best Local Similarity 25.7%; Pred. NO. 45;
Matches 28; Conservative 21; Mismatches 32; Indels 28; Gaps 6;

QY 28 EMSIQLEPYLEENARALEELELRTALQTLQRTVGTTEAGS---LQADPSAETP-TPRGS 83
DB 866 EITRDIPNVEEALRHIDEV---GLII-----VGAELKADILVGKVTTPSESITPEEK 917
QY 84 LKRALNGOD-----SNTVLVS-RLIARTRKORQHGAPE 116
DB 918 LKRALFEKAFDYKDSLSLHVPSGSGTVEVRIEFSRGVKKDQRAIAIE 966

RESULT 13
EAD_EBV
ID EAD_EBV STANDARD; PRT; 404 AA.
AC P03191;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Early antigen protein D (EA-D).
GN BMRE1.
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.

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OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Banker A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Sachdev S.C., Seglin C.,
RA Tufnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [2]
RP SEQUENCE OF 123-404 FROM N.A.
RX MEDLINE=87284177; PubMed=2441081;
RA Pfizner A.J., Strominger J.L., Speck S.H.;
RT "Characterization of a cDNA clone corresponding to a transcript from
RT the Epstein-Barr virus BamHI M fragment: evidence for overlapping
RT mRNAs.";
RL J. Virol. 61:2943-2946(1987).
RN [3]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=86062917; PubMed=2994442;
RA Cho M.-S., Milman G., Hayward S.D.;
RT "A second Epstein-Barr virus early antigen gene in BamHI fragment M
RT encodes a 48- to 50-kilodalton nuclear protein.";
RL J. Virol. 56:860-866(1985).
CC -I- FUNCTION: TRANS-ACTIVATOR FOR LYTIC CYCLE.
CC -I- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL; V01555; CA24844.1; -
DR EMBL; M17322; AAA4587.1; -
DR PIR; A03754; Q08B13.
DR PIR; S32998; S32998.
KW Early protein: Transcription regulation: Activator: DNA-binding;
KW Nuclear protein; Antigen.
SQ SEQUENCE 404 AA; 43373 MW; 533B5D5ECC05F960 CRC64;

Query Match 11.5%; Score 72.5; DB 1; Length 404;
Best Local Similarity 24.8%; Pred. NO. 12;
Matches 34; Conservative 12; Mismatches 54; Indels 37; Gaps 4;

QY 17 PLSPSPV-----TDTGEMSLQPLVY-----ENALRALELE----- 48
DB 258 PAVSVPIRLREYRSGLIIVAGLLTSAGDLPDLDSVLIFFNHAASEAASTASEPDKSPRV 317
QY 49 -----RTALLQTLQRTVGTTEAGSLQADPSAETP-TPRGSRLKALGQDSNTVLSPLLA--- 102
DB 318 QPLGTGLQQRBRHIVSPSPPPPPPTMTESPARPETPSAIPRSHSSNTALERPLAVOL 377
QY 103 ---RTRKORQHGAPE 116
DB 378 ARKRTSSEAROKOKHPK 394

RESULT 14
POBI_YEAST
ID POBI_YEAST STANDARD; PRT; 926 AA.
AC O01454;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA polymerase alpha-binding protein (POBI/CTF4 protein) (Chromosome
DE replication protein CHL15).
GN POBI OR CTF4 OR CHL15 OR YPR135W OR P9659.7.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

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SQ SEQUENCE 920 AA: 100862 MW: E55FE69E8750A4B4 CRC64;
 Query Match 11.4%; Score 72; DB 1; Length 920;
 Best Local Similarity 31.2%; Pred. No. 35;
 Matches 40; Conservative 9; Mismatches 47; Indels 32; Gaps 7;
 QY 2 DRVPCCLLFVGL-----NPLSFVPTDTGEMSLQLPVLEENALRALEELE----- 48
 DB 723 DRI-----VGLIERDFIRGPADDPQVTDGRLLR--IYSESDLVIAECLRTGAMAG 773
 QY 49 -RTALLQTLRQYVGTAEESLGADP-SAEPTPRGSLRKALTGODSNTVLSRLARTRK 106
 DB 774 LRPALAAVSAVLEYTRGDDGPGGVPDAEAPTPR--LRQALQH-----TSRLSATLRA 825
 QY 107 ORKQHGTA 114
 DB 826 DEQRHRIA 833

Search completed: March 10, 2003, 17:39:20
 Job time : 7.98108 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:35:28 ; Search time 23.6027 Seconds

(Without alignments)
1073.767 Million cell updates/sec

Title: US-09-831-907a-30

Perfect score: 633
Sequence: 1 MDRVPPCCLLFVGLINPLLS.....TRKORQHGTAPCECFWYCI 123

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_21:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhnc:*
9: sp_organellae:*
10: sp_phage:*
11: sp_plant:*
12: sp_protent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rvirts:*
17: sp_bacteriap:*
17: sp_cheap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	243.5	38.5	121	6	Q95J46
2	234	37.0	139	4	Q8TAU6
3	163.5	25.8	85	6	Q95K72
4	85.5	13.5	783	16	Q92B19
5	81	12.8	470	5	Q9W249
6	80.5	12.7	783	16	Q9W249
7	77.5	12.2	323	2	Q9WY75
8	77.5	12.2	760	16	Q9RXG0
9	77	12.2	850	5	Q44090
10	77	12.2	850	5	Q44090
11	76.5	12.1	582	4	Q9VM02
12	75.5	11.9	323	2	Q8VWK5
13	75	11.8	272	4	Q9B019
14	75	11.8	478	4	Q00153
15	74.5	11.8	468	16	Q9A8X8
16	74.5	11.8	708	16	Q9PEZ6

17	74	11.7	270	2	Q9AMES	Q9AMES desulfovibr
18	74	11.7	517	11	Q99K04	Q99K04 mus musc
19	74	11.7	2399	16	Q8U9P4	Q8U9P4 agrobacteri
20	73.5	11.6	297	11	Q359Z9	Q359Z9 mus muscu
21	73.5	11.6	1144	5	P91389	P91389 caenorhabdi
22	73	11.5	478	11	Q8VDL2	Q8VDL2 mus muscu
23	73	11.5	478	11	Q8R5L2	Q8R5L2 mus muscu
24	73	11.5	538	5	Q9VIR6	Q9VIR6 drosophila
25	73	11.5	823	2	P74862	P74862 drosophila
26	73	11.5	920	16	Q8Z6K9	Q8Z6K9 salmone
27	73	11.5	920	16	Q8Z6P5	Q8Z6P5 salmone
28	73	11.5	2362	5	Q9NGR9	Q9NGR9 salmone
29	72	11.4	240	2	Q9F0V5	Q9F0V5 drosophila
30	72	11.4	274	10	Q8RVE3	Q8RVE3 azaricus sp
31	72	11.4	1289	2	Q9F0C7	Q9F0C7 oryza sativ
32	72	11.4	2517	5	Q9M060	Q9M060 drosophila
33	71.5	11.3	297	16	Q8Y092	Q8Y092 ralsiona s
34	71.5	11.3	404	16	Q9K0B4	Q9K0B4 vibrio chol
35	71.5	11.3	886	10	Q9SLN1	Q9SLN1 arabidopsi
36	71.5	11.3	893	16	Q9XIV4	Q9XIV4 thermotoga
37	71.5	11.3	939	16	Q8ZJ68	Q8ZJ68 yersinia pe
38	71	11.2	331	16	Q8REI3	Q8REI3 fusobacteri
39	71	11.2	380	3	Q8TFH7	Q8TFH7 schizosacch
40	71	11.2	426	10	Q9S0T6	Q9S0T6 arabidopsi
41	71	11.2	455	11	Q920L8	Q920L8 mus muscu
42	71	11.2	535	11	Q9E0T7	Q9E0T7 mus muscu
43	71	11.2	570	16	Q8ZP20	Q8ZP20 salmone
44	71	11.2	574	5	Q9BLN0	Q9BLN0 leishmania
45	71	11.2	602	11	Q91YD3	Q91YD3 mus muscu

ALIGNMENTS

RESULT 1
ID Q95J46 PRELIMINARY: PRT: 121 AA.
AC Q95J46;
DT 01-DEC-2001 (TREMUREL, 19, Created)
DT 01-DEC-2001 (TREMUREL, 19, Last sequence update)
DT 01-MAR-2002 (TREMUREL, 20, Last annotation update)
DE Urotensin II transcript variant 1.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN 11;
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Sugo T., Mori M.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN 12;
RP SEQUENCE FROM N.A.
RC TISSUE=SPINAL CORD;
RA Mori M., Sugo T., Abe M., Shimomura Y., Kurihara M., Kitada C.,
RA Kikuchi K., Shintani Y., Kurokawa T., Onda H., Nishimura O.,
RA Fujino M.;
RT "Urotensin II is the endogenous ligand of a G-protein-coupled orphan
RT receptor, SENR (GPR14).";
RL Biochem. Biophys. Res. Commun. 265:123-129(1999).
DR EMBL: AB063245; BAB60888.1; -;
DR EMBL: AB063244; BAB60887.1; -;
DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II; 1.
DR PROSITE: PS00984; UROTENSIN_II; UNKNOWN_1.
SQ
SEQUENCE 121 AA: 13580 MW: 6564801AF69101B CRC64;
Query Match 38.5%; Score 243.5; DB 6; Length 121;
Best local Similarity 45.7%; Pred. No. 1.1e-15;
Matches 53; Conservative 15; Mismatches 47; Indels 1; Gaps 1;
QY 8 CLFVGLINPLSPVVDTEGMSIQLPVLENNALALEELRTALQTLRQVGTAEAGS 67

Db 7 CULLLGGCGLGLFALVPDPDSRKEPLPFS-A-PEDVRSAMDELEASLQMLPETPGAEAGD 65
 QY 68 LGQADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKOROHGTAPCEFWKYCI 123
 Db 66 LNEADAGMDIFPRGEMRKAFSGODPNIFLSHLARIKKPYKKRGPPSECFWKYCV 121

RESULT 2

Q8TAU6 PRELIMINARY: PRT; 139 AA.

AC O8TAU6: 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Similar to urotensin 2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=PANCREAS;
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: BC025776; AAH25776.1; -
 SQ SEQUENCE 139 AA; 16276 MW; 32DC52936D5BD6 CRC64;

Query Match 37.0%; Score 234; DB 4; Length 139;
 Best Local Similarity 47.4%; Pred. No. 1e-14;
 Matches 55; Conservative 17; Mismatches 38; Indels 6; Gaps 2;

QY 1 MDVRPCCLLFVGLNPLSPVDTGEMSLQPVLEENALRLALELERTALLQTLROTV 60
 Db 1 MYKLASCCLLFGLFPLPLSLPLDSREISFQLSAPHEPARLTPLELERASLQQLPEML 60
 QY 61 GTEAESLGOADPSAETPTPRGSLRK--ALTGDSNTVLSRLART----RKORQK 110
 Db 61 GAERGDLKKAOSSTNIFNPRGNLRKRFQDFSGDPMILLSHLARLWKRYKKORR 116

RESULT 3

Q9SK72 PRELIMINARY: PRT; 85 AA.

AC 09SK72: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE Urotensin II transcript variant 2.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxId=9823;
 RN 11
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPINAL CORD;
 RA Sugo T., Mori M.;
 RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
 RN 12

RP SEQUENCE FROM N.A.
 RC TISSUE=SPINAL CORD;
 RX MEDLINE=20017983; PubMed=10548501;
 RA Mori M., Sugo T., Abe M., Shlomura Y., Kurihara M., Kitada C.,
 RA Kikuchi K., Shintani Y., Kurokawa T., Onda H., Nishimura O.,
 RA Fujino M.;
 RT "Urotensin II is the endogenous ligand of a G-protein-coupled orphan
 receptor, SENR (GPR14)."
 RL Biochem. Biophys. Res. Commun. 265:123-129(1999).
 DR EMBL: AB063246; BAB60889.1; -
 DR InterPro: IPR001483; Urotensin_II.
 DR Pfam: PF02083; Urotensin_II.1.
 DR PROSITE: PS00964; UROTENSIN_II; UNKNOWN_1.
 SQ SEQUENCE 85 AA; 9644 MW; F519CFDEFCBAA863 CRC64;

Query Match 25.8%; Score 163.5; DB 6; Length 85;
 Best Local Similarity 31.9%; Pred. No. 2.8e-08;
 Matches 37; Conservative 11; Mismatches 31; Indels 37; Gaps 1;

QY 8 CLFVGLNPLSPVDTGEMSLQPVLEENALRLALELERTALLQTLROTVGTEAGS 67
 Db 7 CULLLGGCGLGLFALVPDPDSRKEPLP----- 32

QY 68 LGQADPSAETPTPRGSLRKALTGODSNTVLSRLARTRKOROHGTAPCEFWKYCI 123
 Db 33 ---SDAGMDIFPRGEMRKAFSGODPNIFLSHLARIKKPYKKRGPPSECFWKYCV 85

RESULT 4

Q92B19 PRELIMINARY: PRT; 783 AA.

AC 092B19: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hypothetical protein lin1560.
 GN LIN1560.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCBI_TaxId=1642;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP 11262 / SEROVAR 6A;
 RX PubMed=11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusnok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetoui F., Couve E., de Daruvar A., Denoux P.,
 RA Dommann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
 RA Entian K.-D., Fshni H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kretz J., Kuhn M., Kunst F., Kurapkai G.,
 RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstrik G., Novellia S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*."
 RL Science 294:849-852(2001).
 DR EMBL: AL596169; CAC96791.1; -
 DR ListList; LIN01560; -
 DR InterPro: IPR003156; DHNA1.
 DR InterPro: IPR001667; Psesterase.
 DR InterPro: IPR004610; RecT.
 DR Pfam: PF01368; DHH; 1.
 DR Pfam: PF02272; DHNA1; 1.
 DR TIGRFams: TIGR00644; recJ; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 783 AA; 87598 MW; ECO4A20500A688AB CRC64;

Query Match 13.5%; Score 85.5; DB 16; Length 783;
 Best Local Similarity 31.9%; Pred. No. 9.7;
 Matches 37; Conservative 16; Mismatches 36; Indels 27; Gaps 6;

QY 9 LIFVGLNPLSPVDTGEMSLQPV--LEENALRLALELERTALL---QTLROTVG-- 61
 Db 221 LVAVGVAVDLVS--LTIDENRLVQGLIROLRENANIGLAVLAKASLKEAEETIGFG 278

QY 62 ---TEAEGSLGOADPSAET---TPTPRGSLRKALTGODSNTVLSRLARTRKORQK 110
 Db 279 LAIRLNAVGRGLPADRADLLLTDEPEALFLAEIIDDAN-----KERKQ 323

RESULT 5

Q9W249 PRELIMINARY: PRT; 470 AA.

ID 09W249: 01-MAY-2000 (TREMBlrel. 13, Created)

304 NIGGJGKKRPLLGVPRSSHNPTKR-----TWMS-LIARAKNSQALH 424

Submitted (MAY-1999) to the *Journal of Virology*

Submitted (MAY-1999) to the *Journal of Virology*

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RN [2]
RP SEQUENCE FROM N.A.
RC PLASMITID=PMW0;
RA Genka H., Nagata Y., Tsuda M.;
RT "Site-specific resolution system encoded by toluene catabolic
   transposon Tn4651."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151431; AAD44277.1; -
DR EMBL; AB077820; BAB83832.1; -
DR InterPro: IPR002104; Phage_integrase.
DR InterPro: IPR004107; Phage_integr_N.
DR Pfam; PF02899; Phage_integr_N; 1.
KW Plasmid.
SQ SEQUENCE 323 AA; 35835 MW; 8128EE6FDC97CDB8 CRC64;

Query Match 12.2%; Score 77.5; DB 2; Length 323;
Best Local Similarity 31.2%; Pred. No. 20;
Matches 29; Conservative 12; Mismatches 39; Indels 13; Gaps 3;

QY 33 LPVLEENALAELEETALLQTLRQTVGEAGSLGQADPS-AETPTPR-----GSLR 85
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 35 LPATSDNIVIVIEYVATPLSLSTLKQRLALAQWHITQGFDPPTKPTVQVILKIGRTLH 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 86 KALTGQDSNTVLSRL-----LAFTRKQRKQHG 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 95 PAQTKQAAPLQHLQALQALQALQALQALQALQALQALQALQALQALQALQALQ 127
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q9RXG0 PRELIMINARY; PRT; 760 AA.
ID 09RXG0;
AC 09RXG0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RIBONUCLEASE.
GN DR0353.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RL;
RX MEDLINE=20036895; PubMed=10567265;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
   radiodurans RL."
RL Science 286:1571-1577(1999).
DR EMBL; AE001895; AAF09933.1; -
DR TIGR; DR0353; -
DR InterPro: IPR004476; 3_prime_RNase.
DR InterPro: IPR001900; Ribonuclease_II.
DR InterPro: IPR003029; S1.
DR Pfam; PF00773; RNB; 1.
DR Pfam; PF00575; SL; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMs; TIGR00358; 3_prime_RNase; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
KW Complete proteome.
SQ SEQUENCE 760 AA; 84741 MW; 1585C0779A8746E3 CRC64;

Query Match 12.2%; Score 77.5; DB 16; Length 760;
Best Local Similarity 27.8%; Pred. No. 54;
Matches 32; Conservative 15; Mismatches 39; Indels 29; Gaps 5;

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QY 23 VYDTGEMSLQPLVLEENALAELEERT-----LLOTLRQT 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 433 VDKDGMEL-IPIRETAGMEDLMLANKVVAHLIERETPTLRIHEEPLQKFQDV 491
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 VGEAGSLGQADPSAETPTPRG--SLRKALTGQDSNTVLSRLLAETRKQRKQHG 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 492 TG--ATGRLEGFSPGGE-PTPQAVQAVLKQVKGRTGKESVNTLLSMQAKYAG 543
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q44090 PRELIMINARY; PRT; 850 AA.
ID 044090;
AC 044090;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE GTPase activating protein for RAPI.
GN RAPGAP1 OR CG6682.
OS Drosophila melanogaster (Fruit fly).
OC Drosophila melanogaster; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE-IMAGINAL DISC;
RA Chen F., Barkett M., Ram K.T., Quintanilla A., Hartharan I.K.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF023478; AAB87873.1; -
DR FlyBase; FBgn0014015; Rapgap1.
DR InterPro: IPR003880; Rap_gap_attach.
DR InterPro: IPR000331; Rap_GAP.
DR Pfam; PF02145; Rap_GAP; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN.1.
SQ SEQUENCE 850 AA; 92879 MW; 0D0855F88CB76B3 CRC64;

Query Match 12.2%; Score 77; DB 5; Length 850;
Best Local Similarity 29.0%; Pred. No. 68;
Matches 38; Conservative 11; Mismatches 52; Indels 30; Gaps 6;

QY 2 DRVPPCLLFVGLNPLPLSPVY-----DTGEMSLQPLVLEEN-----LRALEELERT 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 480 DVPF-----FGPTLPNAVPRKQGFKEFLTKRLINENACRYAKFAKLEQRRT 531
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 51 ALLQTLRQTVGEAGSLGQ--ADPSAETPTPRGSLRKALTGQDSN-----TVLSRL 101
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 532 SLQWLQCELRKTRDFGLTSLQTSAGSPRP--ETPRAESGSGNAGSRPDTYTKALI 589
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 102 ARTRKQRKQHG 112
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 590 MVRRSQSVDTG 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
Q9VM02 PRELIMINARY; PRT; 850 AA.
ID 09VM02;
AC 09VM02;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE RAPGAP1 protein.
GN RAPGAP1 OR CG6682.
OS Drosophila melanogaster (Fruit fly).
OC Drosophila melanogaster; Tracheata; Hexapoda; Insecta;
OC Eukaryota; Metazoa; Arthropoda; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sultion G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abrell J.F., Agdayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boshakov S.,
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Fleischmann W.,
 RA Giodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gdbbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003617; AAF52526.1; -
 DR FlyBase: FBgn0014015; Rappaport.
 DR InterPro: IPR003880; Ppantne_attach.
 DR Pfam: PF02145; Rap_GAP.
 DR PROSITE: PS00012; PHOSPHOPANTETHEINE: UNKNOWN.1.
 DR SEQUENCE: 850 AA; 92893 MW; 47E7F0483CB76BB3 CRC64;

Query Match 12.2%; Score 77; DB 5; Length 850;
 Best Local Similarity 29.0%; Pred. No. 68;
 Matches 38; Conservative 11; Mismatches 52; Indels 30; Gaps 6;

OY 2 DRVPECLLFVGLNPLSFVPT-----DTGEMSLQPLVEENA-----LRLALELERT 50
 DB 480 DDDVP-----FGPTLPNPAVFRKGQEFKFIILKLINAENACKAKKALEORTRT 531
 OY 51 ALLQTLRQVTGEAGSGISGO--ADPSAEPTPTRGSLRKALTGQDSN-----TVLSRL 101
 DB 532 SLLQWLCELRKTRDFTGLDLSQTSAGSPPT--ETPKAESGSGNAGSRFTDVTYKKALI 589
 OY 102 ATRRQRRQHG 112
 DB 590 MRVRSQSVDTG 600

RESULT 11
 OGNP16 PRELIMINARY; PRT; 582 AA.
 AC OGNP16;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Transcription factor (CDNA FLJ11107 f1s, clone PLACE1005803) (SMIF gene).
 DE SMIF.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PANCREAS;
 RC BAI R.Y., Ouyang T., Hahn S., Peschel C., Dwyer J.;
 RT "SMAD4-interacting transcription factor";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Isogai K., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
 RA Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
 RA Nakamura Y., Nagahara K., Masuno Y., Sasaki N.;
 RT "NEO human cDNA sequencing project";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ275986; CAB77023.1; -
 DR EMBL: AK001959; BAA92008.1; -
 DR EMBL: BC007439; AAH07439.1; -
 DR SEQUENCE: 582 AA; 63278 MW; 26480D0B10CE7C72 CRC64;

Query Match 12.1%; Score 76.5; DB 4; Length 582;
 Best Local Similarity 27.1%; Pred. No. 49;
 Matches 35; Conservative 14; Mismatches 45; Indels 35; Gaps 5;

OY 16 NPLSPFVPTDGEMLQPLVEENALRLALELERTA-----LQTLR----- 57
 DB 353 SPLNQVPELSHSL-----IANOSPFRAPLNTVTAAGTSLPSVLDLQRLRTPHQDIQT 409
 OY 58 QTVG-----TEAGSLGQADPSAETPTPRGSLRKALTGQDSNVTLSRLARTRRQK 109
 DB 410 QPLCKGAMVASFSPAQQLATPESFTPEPKTAARVAASASLSNVLAIP-----QSM 463
 OY 110 OHGTAPCEP 118
 DB 464 QQNDPEVF 472

RESULT 12
 O8YMK5 PRELIMINARY; PRT; 323 AA.
 ID O8YMK5;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Putative cointegrate resolution protein S.
 OS Pseudomonas putida.
 OG Plasmid pMW0.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Greated A., Lamberton L., Williams P.A., Thomas C.M.;
 RT "Complete nucleotide sequence of IncP-9 plasmid pMW0.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ344068; CAC86784.1; -
 DR InterPro: IPR002104; Phage_integrase.
 DR InterPro: IPR004107; Phage_integrase.
 DR Pfam: PF00589; Phage_integrase; 1.
 DR Pfam: PF02899; Phage_integr_N; 1.
 KW Plasmid.

Query Match 11.9%; Score 75.5; DB 2; Length 323;
 Best Local Similarity 31.2%; Pred. No. 30;
 Matches 29; Conservative 11; Mismatches 40; Indels 13; Gaps 3;

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OY 33 LPVLEENALRALEELERTALLQTLRQTVGTEAGSLGQADPS-AETPTPR-----GSLR 85
DB 35 LPPTSNIRALRYVEADTSLSTSLKORLAALQOMHITGFPDPTKPTVROVLKGIPTLH 94
OY 86 KALVGDSNTVLSRL-----LARTKOKRKHG 112
DB 95 PAOTKQAPLQLOHLEQATQWLSREAEQAQOQSG 127

RESULT 13
O9B019 PRELIMINARY: PRT: 272 AA.
AC O9B019:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to clones 23667 and 23775 zinc finger protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strauberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strauberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Strauberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004357; AAH04357.1; -.
DR EMBL: BC000330; AAH00330.1; -.
DR InterPro: IPR000822; Znf.C2H2.
DR Pfam: PF00096; Zf-C2H2.1.
DR SMART: SM00355; Znf.C2H2.1.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 1.
DR DNA-binding; Zinc-finger.
KW DNA-binding; Zinc-finger.
SQ SEQUENCE 272 AA; 29761 MW; B3A06732DA0C01F8 CRC64;

Query Match 11.8%; Score 75; DB 4; Length 272;
Best Local Similarity 31.8%; Pred. No. 28;
Matches 28; Conservative 15; Mismatches 39; Indels 6; Gaps 3;

OY 22 PVTDTGEMS-LQLPVLEENALRALEELERTALLQTLRQTVGTEAGSLGQADPSAET 77
DB 43 PVTSEASCSRLMLPDDTTNHSNSKREVPSSAVLSRLVNGPDEETRAQTVOKSPFELS 102
OY 78 PTPRGSRLKALVGDSNTVLSRLAATR 105
DB 103 TSESSSLQDLPQSDSTSF1--LLNLTR 128

RESULT 14
O00153 PRELIMINARY: PRT: 478 AA.
AC O00153:
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Zinc finger protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA MEDLINE=96307227; PubMed=8619474;
RA Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.;
RT "A 'double adaptor' method for improved shotgun library

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RT construction.";
RL Anal. Biochem. 236:107-113(1996).
RN 12
RP SEQUENCE FROM N.A.
RC TISSUE=BRIN;
RA Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,
RA Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.;
RT "Large-scale concatenation cDNA sequencing."
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL: U09019; AAB51059.1; -.
DR HSSP: P08047; 1SP2.
DR InterPro: IPR000822; Znf.C2H2.
DR Pfam: PF00096; Zf-C2H2.5.
DR PRINTS: PR00048; ZINC_FINGER.
DR SMART: SM00355; Znf.C2H2.5.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 5.
DR DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SQ SEQUENCE 478 AA; 52113 MW; 107E7E139618F863 CRC64;

Query Match 11.8%; Score 75; DB 4; Length 478;
Best Local Similarity 31.8%; Pred. No. 54;
Matches 28; Conservative 15; Mismatches 39; Indels 6; Gaps 3;

OY 22 PVTDTGEMS-LQLPVLEENALRALEELERTALLQTLRQTVGTEAGSLGQADPSAET 77
DB 43 PVTSEASCSRLMLPDDTTNHSNSKREVPSSAVLSRLVNGPDEETRAQTVOKSPFELS 102
OY 78 PTPRGSRLKALVGDSNTVLSRLAATR 105
DB 103 TSESSSLQDLPQSDSTSF1--LLNLTR 128

RESULT 15
O9A8X8 PRELIMINARY: PRT: 468 AA.
AC O9A8X8:
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Oxidoreductase, FAD-binding.
DE CC1219.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA Deboy R.T., Dodson R.D., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Ueberlack T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RL EMBL: AE005798; AAK23201.1; -.
DR TIGR: CC1219; -.
DR InterPro: IPR001575; Oxid_FAD_bind.
DR Pfam: PF01565; FAD_binding_4; 1.
KW Complete proteome.
SQ SEQUENCE 468 AA; 51112 MW; F8B8574BE13768C3 CRC64;

Query Match 11.8%; Score 74.5; DB 16; Length 468;
Best Local Similarity 37.7%; Pred. No. 58;
Matches 29; Conservative 9; Mismatches 32; Indels 7; Gaps 3;

OY 28 EMSLQPVLEENALRALEELERTALLQTLRQTVGTEAGSLGQADPSAET---TPRGS 84
DB 103 TSESSSLQDLPQSDSTSF1--LLNLTR 128

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Page 7

Db	337	EMEFHLPV-ENQKALEEVMRT--ITERPDVFPPIEVRIADDMISPPYAPRGSV	392
Qy	85	RKALTGODSNTVLSRL	101
Db	393	AVHAYYRDDEFTFELYELI	409

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Job time : 25.6027 secs

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XX  Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H:
PI  WPI: 2000-400075/34.
XX  N-PSDB; AAA46719.
XX  New mammalian urotensin II polypeptide, useful for treating
PI  neurodegeneration and spinal cord injury -
XX  Claim 2; Page 31; 42pp; French.
XX  The present sequence represents a murine prepro-urotensin II polypeptide.
CC  In mammals, urotensin II promotes survival and regeneration of motor
CC  neurons, and also has a hypertensive effect. The urotensin II
CC  polypeptides and polynucleotides are useful for treating
CC  neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
CC  para-plegia or amyotrophic lateral sclerosis). The polypeptides
CC  are also used to screen for specific inhibitors, i.e. potential
CC  antihypertensive agents.
XX  SQ  Sequence 123 AA:
XX
Query Match 100.0%; Score 641; DB 21; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRVPCCLFTGLNPLSLPVTDTGERTLQPLVEEDALRALLEELERMALLQTLRQTM 60
DB 1 MDRVPCCLFTGLNPLSLPVTDTGERTLQPLVEEDALRALLEELERMALLQTLRQTM 60
QY 61 GTEAGSGPGAGPSTETPTPRGSMRKAFAQNSNTVLSRLATRTKQKHGAAPCEFWK 120
DB 61 GTEAGSGPGAGPSTETPTPRGSMRKAFAQNSNTVLSRLATRTKQKHGAAPCEFWK 120
QY 121 YCI 123
DB 121 YCI 123
DB 121 YCI 123
XX
RESULT 2
AAB60445
ID AAB60445 standard; Protein: 123 AA.
XX
AC AAB60445;
XX
DT 24-APR-2001 (first entry)
XX
DE Mouse urotensin II-like peptide precursor protein, SEQ ID NO:26.
XX
KW Urotensin II-like peptide; precursor protein; mouse; murine; SENR ligand;
KW drug screening; sensory epithelium neuropeptide-like receptor;
KW diagnosis; central nervous function; cardiac function;
KW circulatory function.
XX
OS Mus sp.
XX
PN WO200104298-A1.
XX
PD 18-JAN-2001.
XX
PF 06-JUL-2000; 2000WO-JP04484.
XX
PR 08-JUL-1999; 93JP-0194091.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Sugo T, Kurihara M, Kitaoka C, Mori M;
XX
DR WPI: 2001-147192/15.
XX  N-PSDB; AAF59584.
XX
PT Urotensin II-like peptide originating in rat or mouse and encoded
PT nucleic acid, useful in study of its physiological effects, for

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PI diagnosis and development of drugs for controlling e.g. central nervous
PI function -
XX
PS Claim 5; Page 99; 110pp; Japanese.
XX
XX  The invention relates to novel rat and mouse urotensin II-like peptide
CC  (AAB60443-AAB60444, AAB60446, AAB60449-AAB60452), their amides, esters
CC  or salts, their precursor proteins (AAB60442, AAB60445), and to nucleic
CC  acids encoding the urotensin II-like peptides (AAFS9575-AAFS9576,
CC  AAF59585-AAFS9588) or the urotensin II-like peptide protein precursors
CC  (AAFS9574, AAF59584). The urotensin II-like peptides are ligands of the
CC  sensory epithelium neuropeptide-like receptor (SENR). The invention also
CC  relates to vectors and transformants comprising the novel nucleic acid
CC  sequences, the recombinant production of the rat or mouse urotensin II-
CC  like peptides or their precursors, an antibody against a urotensin II-
CC  like peptide or precursor, a method of screening for compounds which can
CC  modulate the binding of urotensin II-like peptides to the SENR, the
CC  compounds thus identified, and a method of quantitating urotensin II-like
CC  peptides or their precursors. The peptides and proteins, and nucleic
CC  acids encoding them are useful in study of the physiological effects of
CC  urotensin II-like peptide/SENR interactions, and for the diagnosis and
CC  development of drugs (including gene therapy compositions) for modulating
CC  e.g., central nervous function, cardiac function and circulatory
CC  function. The present sequence represents the mouse urotensin II-like
CC  peptide precursor protein of the invention.
XX  SQ  Sequence 123 AA:
XX
Query Match 100.0%; Score 641; DB 22; Length 123;
Best Local Similarity 100.0%; Pred. No. 3.1e-62;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDRVPCCLFTGLNPLSLPVTDTGERTLQPLVEEDALRALLEELERMALLQTLRQTM 60
DB 1 MDRVPCCLFTGLNPLSLPVTDTGERTLQPLVEEDALRALLEELERMALLQTLRQTM 60
QY 61 GTEAGSGPGAGPSTETPTPRGSMRKAFAQNSNTVLSRLATRTKQKHGAAPCEFWK 120
DB 61 GTEAGSGPGAGPSTETPTPRGSMRKAFAQNSNTVLSRLATRTKQKHGAAPCEFWK 120
QY 121 YCI 123
DB 121 YCI 123
DB 121 YCI 123
XX
RESULT 3
AAB60124
ID AAB60124 standard; Protein: 123 AA.
XX
AC AAB60124;
XX
DT 07-OCT-2002 (first entry)
XX
DE Mouse urotensin II-like peptide #1.
XX
KW SENR; sensory epithelium neuropeptide-like receptor; mouse; fear;
KW attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
KW schizophrenia; G protein-coupled; receptor.
XX
OS Mus sp.
XX
PN WO200214513-A1.
XX
PD 21-FEB-2002..
XX
PF 10-AUG-2001; 2001WO-JP06899.
XX
PR 10-AUG-2000; 2000JP-0247968.
XX

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PA (TAKE) TAKEDA CHEM IND LTD.
 XX Matsumoto Y, Watanabe T, Takahashi H, Mori M;
 XX WPI: 2002-329576/36.
 DR N-PSDB; ABR50030.
 XX Polypeptide GPR12 with ligand activity to sensor epithelium
 PT neuropeptide-like receptor, useful e.g. in treating attention deficit
 PT disorder or narcolepsy, or for screening drug candidates for these
 PT indications and for anxiety -
 XX
 PS Claim 6; Page 280; 290pp; Japanese.
 XX
 CC This invention relates to an anti-attention deficit disorder or anti-
 CC narcolepsy agent containing a polypeptide with a sequence identical or
 CC substantially similar to a fully defined 12 amino acid sequence given in
 CC the specification, and its amide, ester or their salt. The peptides
 CC have ligand activity to sensory epithelium neuropeptide-like receptor
 CC (SENR) protein. The invention also includes a method for diagnosing
 CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
 CC schizophrenia or fear. The polypeptides of the invention, their
 CC precursor proteins and their encoding DNAs are useful in treating
 CC attention deficit disorder or narcolepsy, or for screening drug
 CC candidates for these indications and for anxiety, depression, insomnia,
 CC schizophrenia or fear. They are also useful for gene therapy. The
 CC polypeptide is a G protein-coupled receptor protein, with ligand
 CC activity to sensor epithelium neuropeptide-like receptor. The present
 CC sequence represents the mouse neurotensin II-like peptide of the
 CC invention.
 XX
 SQ Sequence 123 AA:
 Query Match 100.0%; Score 641; DB 23; Length 123;
 Best Local Similarity 100.0%; Pred. No. 3.1e-62;
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDRVPECLLFIGLNLPLSPVTDGERTLQLPVLEEDALRALEELERALLQTLRQTM 60
 DB 1 MDRVPECLLFIGLNLPLSPVTDGERTLQLPVLEEDALRALEELERALLQTLRQTM 60
 QY 61 GTEAGESPGEAGPSTETPTPRGSMKRAFAGONSNTVLSRLIARRKQKHGAAPCECFWK 120
 DB 61 GTEAGESPGEAGPSTETPTPRGSMKRAFAGONSNTVLSRLIARRKQKHGAAPCECFWK 120
 QY 121 YCI 123
 DB 121 YCI 123
 RESULT 4
 AAY93644
 ID AAY93644 standard; Protein: 123 AA.
 AC AAY93644;
 DT 25-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of rat prepro-urotensin II (UII) polypeptide.
 XX
 KW Urotensin II: motor neuron; hypertensive; neurodegeneration;
 KW spinal cord trauma; hemi-plegia; para-plegia;
 KW amyotrophic lateral sclerosis; antihypertensive agent.
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note="signal peptide"
 FT Peptide 21..109
 FT /note="pro-segment peptide"
 FT Peptide 110..123
 FT /note="urotensin II peptide"

XX
 PN WO200031265-A1.
 XX
 PD 02-JUN-2000.
 XX
 PF 26-NOV-1999; 99WO-FR02941.
 XX
 PR 26-NOV-1998; 98FR-0014914.
 XX
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 XX
 PI Beauvillain J, Coulouarn Y, Jegou S, Lohrmann I, Vaudry H;
 PI WPI: 2000-400075/34.
 DR N-PSDB; AAA46710.
 XX
 PT New mammalian urotensin II polypeptide, useful for treating
 PT neurodegeneration and spinal cord injury -
 XX
 PS Disclosure; Page 30; 42pp; French.
 XX
 CC The present sequence represents a rat prepro-urotensin II polypeptide.
 CC In mammals, urotensin II promotes survival and regeneration of motor
 CC neurons, and also has a hypertensive effect. The urotensin II
 CC polypeptides and polynucleotides are useful for treating
 CC neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
 CC para-plegia or amyotrophic lateral sclerosis). The polypeptides
 CC are also used to screen for specific inhibitors, i.e. potential
 CC antihypertensive agents.
 XX
 SQ Sequence 123 AA:
 Query Match 84.4%; Score 541; DB 21; Length 123;
 Best Local Similarity 84.6%; Pred. No. 2.7e-51;
 Matches 104; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MDRVPECLLFIGLNLPLSPVTDGERTLQLPVLEEDALRALEELERALLQTLRQTM 60
 DB 1 MDRVPECLLFVGLNLPLSPVTDGEMSLQLPVLEENALRALEELERALLQTLRQTV 60
 QY 61 GTEAGESPGEAGPSTETPTPRGSMKRAFAGONSNTVLSRLIARRKQKHGAAPCECFWK 120
 DB 61 GTEAGESPGEAGPSTETPTPRGSLRKALTGDSNTVLSRLIARRKQKHGAAPCECFWK 120
 QY 121 YCI 123
 DB 121 YCI 123
 RESULT 5
 AAB60442
 ID AAB60442 standard; Protein: 123 AA.
 AC AAB60442;
 DT 24-APR-2001 (first entry)
 XX
 DE Rat urotensin II-like peptide precursor protein, SEQ ID NO:13.
 XX
 KW Urotensin II-like peptide; precursor protein; rat; SENR ligand;
 KW drug screening; sensory epithelium neuropeptide-like receptor;
 KW diagnosis; central nervous function; cardiac function;
 KW circulatory function.
 OS Rattus sp.
 XX
 PN WO200104298-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 06-JUL-2000; 2000WO-JP04484.
 XX
 PR 08-JUL-1999; 99JP-0194091.

XX (TAKE) TAKEDA CHEM IND LTD.
 PA Sugo T, Kurihara M, Kitada C, Mori M;
 PI MPI: 2001-147192/15.
 XX N-PSDB: AAF59574.
 DR
 XX Urotensin II-like peptide originating in rat or mouse and encoded
 PT nucleic acid, useful in study of its physiological effects, for
 PT diagnosis and development of drugs for controlling e.g. central nervous
 PT function -
 XX
 PS Claim 5; Page 95; 110pp; Japanese.
 XX
 XX The invention relates to novel rat and mouse urotensin II-like peptide
 CC (AAB60443-AAB60444, AAB60445-AAB60452), their amides, esters
 CC or salts, their precursor proteins (AAB60442, AAB60443), and to nucleic
 CC acids encoding the urotensin II-like peptides (AAF59575-AAF59576,
 CC AAF59585-AAF59589) or the urotensin II-like peptide protein precursors
 CC (AAF59574, AAF59584). The urotensin II-like peptide are ligands of the
 CC sensory epithelium neuropeptide-like receptor (SENR). The invention also
 CC relates to vectors and transformants comprising the novel nucleic acid
 CC sequences, the recombinant production of the rat or mouse urotensin II-
 CC like peptides or their precursors, an antibody against a urotensin II-
 CC like peptide or precursor, a method of screening for compounds which can
 CC modulate the binding of urotensin II-like peptides to the SENR, the
 CC compounds thus identified, and a method of quantitating urotensin II-like
 CC peptides or their precursors. The peptides and proteins, and nucleic
 CC acids encoding them are useful in study of the physiological effects of
 CC urotensin II-like peptide/SENR interactions, and for the diagnosis and
 CC development of drugs (including gene therapy compositions) for modulating
 CC e.g., central nervous function, cardiac function and circulatory
 CC function. The present sequence represents the rat urotensin II-like
 CC peptide precursor protein of the invention.
 CC
 SQ Sequence 123 AA:
 Query Match 84.4%; Score 541; DB 22; Length 123;
 Best Local Similarity 84.6%; Pred. No. 2.7e-51;
 Matches 104; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MDRVPCCLLFGLNPLSLPYDTGERTLOLVLEEDALRALLEERALLQTLKQTM 60
 DB 1 MDRVPCCLLFGLNPLSLPYDTGERTLOLVLEEDALRALLEERALLQTLKQTV 60
 QY 61 GTEAGSPGCEAGSTETPTPRGSMKAFACQNSNTVLSRLARTRKOHKOGAARECFWK 120
 DB 61 GTEAGSLGAGDSAEPTPRGSLRKALITGDSNTVLSRLARTRKOROHGTAPECFWK 120
 QY 121 YCI 123
 DB 121 YCI 123
 RESULT 6
 AA080121
 ID AA080121 standard; Protein; 123 AA.
 AC AA080121;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Rat sensory epithelium neuropeptide-like receptor (SENR) protein.
 XX
 KW SENR, Sensory epithelium neuropeptide-like receptor; rat; fear;
 KM attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
 XX schizoprenia; G protein-coupled; receptor.
 OS Rattus sp.
 XX
 PN WO200214513-A1.
 XX

PD 21-FEB-2002.
 XX
 XX 10-AUG-2001; 2001WO-JP06899.
 PF
 XX 10-AUG-2000; 2000JP-0247968.
 PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 PI Matsumoto Y, Watanabe T, Takahashi H, Mori M;
 XX MPI: 2002-329576/36.
 DR
 XX
 XX Polypeptide GPR12 with ligand activity to sensor epithelium
 PT neuropeptide-like receptor, useful e.g. in treating attention deficit
 PT disorder or narcolepsy, or for screening drug candidates for these
 PT indications and for anxiety -
 XX
 PS Claim 6; Page 277-278; 290pp; Japanese.
 XX
 XX This invention relates to an anti-attention deficit disorder or anti-
 CC narcolepsy agent containing a polypeptide with a sequence identical or
 CC substantially similar to a fully defined 12 amino acid sequence given in
 CC the specification, and its amide, ester or their salt. The peptides
 CC have ligand activity to sensory epithelium neuropeptide-like receptor
 CC (SENR) protein. The invention also includes a method for diagnosing
 CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
 CC schizoprenia or fear. The polypeptides of the invention, their
 CC precursor proteins and their encoding DNAs are useful in treating
 CC attention deficit disorder or narcolepsy, or for screening drug
 CC candidates for these indications and for anxiety, depression, insomnia,
 CC schizoprenia or fear. They are also useful for gene therapy. The
 CC polypeptide is a G protein-coupled receptor protein, with ligand
 CC activity to sensor epithelium neuropeptide-like receptor. The present
 CC sequence represents the rat sensory endothelium neuropeptide-like
 CC receptor protein of the invention.
 CC
 SQ Sequence 123 AA:
 Query Match 84.4%; Score 541; DB 23; Length 123;
 Best Local Similarity 84.6%; Pred. No. 2.7e-51;
 Matches 104; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MDRVPCCLLFGLNPLSLPYDTGERTLOLVLEEDALRALLEERALLQTLKQTM 60
 DB 1 MDRVPCCLLFGLNPLSLPYDTGERTLOLVLEEDALRALLEERALLQTLKQTV 60
 QY 61 GTEAGSPGCEAGSTETPTPRGSMKAFACQNSNTVLSRLARTRKOHKOGAARECFWK 120
 DB 61 GTEAGSLGAGDSAEPTPRGSLRKALITGDSNTVLSRLARTRKOROHGTAPECFWK 120
 QY 121 YCI 123
 DB 121 YCI 123
 RESULT 7
 AA93648
 ID AA93648 standard; Protein; 103 AA.
 AC AA93648;
 XX
 DT 25-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of murine pro-urotensin II (UII) polypeptide.
 XX
 KW Urotensin II; motor neuron; hypertensive; neurodegeneration;
 KM spinal cord trauma; hemi-plegia; para-plegia;
 XX amyotrophic lateral sclerosis; antihypertensive agent.
 OS Mus sp.
 XX
 PN Location/Qualifiers
 FT Peptide 1..86
 FT

```
FT      /note= "pro-segment"  
FT      87..103  
FT      /note= "urotensin II"  
XX      WO200031265-A1.  
XX      02-JUN-2000.  
XX      26-NOV-1999; 99WO-FR02941.  
XX      26-NOV-1998; 98FR-0014914.  
XX      (INRM ) INST NAT SANTE & RECH MEDICALE.  
XX      Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;  
XX      WPI; 2000-400075/34.  
XX      N-PSDB; AAA46720.  
XX      New mammalian urotensin II polypeptide, useful for treating  
XX      neurodegeneration and spinal cord injury -  
XX      Claim 2; Page 32; 42pp; French.  
XX      The present sequence represents a murine pro-urotensin II polypeptide.  
XX      In mammals, urotensin II promotes survival and regeneration of motor  
XX      neurons, and also has a hypertensive effect. The urotensin II  
XX      polypeptides and polynucleotides are useful for treating  
XX      neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,  
XX      para-plegia or amyotrophic lateral sclerosis). The polypeptides  
XX      are also used to screen for specific inhibitors, i.e. potential  
XX      antihypertensive agents.  
XX      Sequence 103 AA;  
SQ  
Query Match 83.2%; Score 533; DB 21; Length 103;  
Best Local Similarity 100.0%; Pred. No. 1.6e-50;  
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY      21 LPVTDGERTQLPYLEEDALRALEELERMALLOTLRQTGTEAGSPGSPSTPTTPR 80  
DB      1 LPVTDGERTQLPYLEEDALRALEELERMALLOTLRQTGTEAGSPGSPSTPTTPR 60  
OY      81 RGSNRKAFAGONSNTVLSRLARTRKQKHOGAPECFWKTCI 123  
DB      61 RGSNRKAFAGONSNTVLSRLARTRKQKHOGAPECFWKTCI 103  
RESULT 8  
AA93645  
ID      AA93645 standard; Protein; 103 AA.  
XX      AAY93645;  
XX      25-SEP-2000 (first entry)  
XX      Amino acid sequence of rat pro-urotensin II (U11) polypeptide.  
XX      Urotensin II; motor neuron; hypertensive; neurodegeneration;  
XX      spinal cord trauma; hemi-plegia; para-plegia;  
XX      amyotrophic lateral sclerosis; antihypertensive agent.  
XX      Rattus sp.  
XX      Key Location/Qualifiers  
XX      Peptide 1..89  
XX      FT /note= "pro-segment"  
XX      FT 90..103  
XX      FT Peptide /note= "urotensin II peptide"  
XX      WO200031265-A1.  
XX      02-JUN-2000.
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XX      26-NOV-1999; 99WO-FR02941.  
XX      26-NOV-1998; 98FR-0014914.  
XX      (INRM ) INST NAT SANTE & RECH MEDICALE.  
XX      Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;  
XX      WPI; 2000-400075/34.  
XX      N-PSDB; AAA46711.  
XX      New mammalian urotensin II polypeptide, useful for treating  
XX      neurodegeneration and spinal cord injury -  
XX      Claim 2; Page 30-31; 42pp; French.  
XX      The present sequence represents a rat pro-urotensin II polypeptide.  
XX      In mammals, urotensin II promotes survival and regeneration of motor  
XX      neurons, and also has a hypertensive effect. The urotensin II  
XX      polypeptides and polynucleotides are useful for treating  
XX      neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,  
XX      para-plegia or amyotrophic lateral sclerosis). The polypeptides  
XX      are also used to screen for specific inhibitors, i.e. potential  
XX      antihypertensive agents.  
XX      Sequence 103 AA;  
SQ  
Query Match 67.7%; Score 434; DB 21; Length 103;  
Best Local Similarity 83.3%; Pred. No. 1.1e-39;  
Matches 85; Conservative 6; Mismatches 11; Indels 0; Gaps 0;  
OY      22 PVPDTGERTQLPYLEEDALRALEELERMALLOTLRQTGTEAGSPGSPSTPTTPR 81  
DB      2 PVPDTGEMSLQLPYLEENALRALEELERTALLOTLRQTGTEAGSLGQDPASERTPTPR 61  
OY      82 GSNRKAFAAGONSNTVLSRLARTRKQKHOGAPECFWKTCI 123  
DB      62 GSNRKAFTGDSNTVLSRLARTRKQKHOGTAPECFWKTCI 103  
RESULT 9  
AAB12501  
ID      AAB12501 standard; Protein; 122 AA.  
XX      AAB12501;  
XX      27-OCT-2000 (first entry)  
XX      Bovine SENR ligand protein sequence SEQ ID NO:29.  
XX      SENR; sensory epithelium neuropeptide-like receptor; urotensin II;  
XX      diagnosis; G protein-coupled receptor; hypertension; GPR14; hormone;  
XX      kidney disease; regulator; central function; circulatory function;  
XX      heart function; immune system function; digestive function;  
XX      metabolic function; genital function.  
XX      Bos taurus.  
XX      WO200032627-A1.  
XX      08-JUN-2000.  
XX      29-NOV-1999; 99WO-JP06649.  
XX      30-NOV-1998; 98JP-0338984.  
XX      04-FEB-1999; 99JP-0026848.  
XX      26-AUG-1999; 99JP-0239367.  
XX      (TAKE ) TAKEDA CHEM IND LTD.  
XX      Mori M, Abe M, Shimomura Y, Sugo T, Kitada C;
```

DR WPI: 2000-412287/35.
XX
XX Urotensin peptides which are ligands for sensory epithelium
PT neuropeptide-like receptor (SENR) for diagnosis and treatment of
PT hypertension
XX
XX Example 36; Page 140-141; 147pp; Japanese.
PS
XX The present invention provides peptides which are ligands for sensory
CC epithelium neuropeptide-like receptor (SENR), and their amides, esters
CC and salts. SENR is a G-protein coupled receptor protein (also known as
CC GPR4), and the peptides which are ligands for it are forms of the
CC peptide hormone urotensin II. The peptides can be used in the treatment
CC and diagnosis of hypertension and kidney disease, and the development of
CC drugs which are regulators of central functions, circulatory functions,
CC heart functions, immune system functions, digestive functions, metabolic
CC functions and genital functions. The present sequence represents a
CC bovine SENR ligand protein from the present invention.
XX
SQ Sequence 122 AA;
Query Match 48.8%; Score 312.5; DB 21; Length 122;
Best Local Similarity 52.8%; Pred. No. 2.7e-26;
Matches 65; Conservative 16; Mismatches 41; Indels 1; Gaps 1;
QY 1 MDRVPCCLLFTGLNPLSLPYDTGERTLQPLVEDALRALLELERNALLQTLRQTM 60
DB 1 MYKLVSCLLFTGLSLNPLSLPYLDSRQSLQ-LAPEVRSRLDELERSLLQMLPEMS 59
QY 61 GTFAGSPGEAGSTETPPRGSMRKAFAGQNSNTVLSRLARTRKQHKOHGAAPCFWK 120
DB 60 GAGTGGRLNTDPTITNIFYPRGMRRKAFSGQDPKFLSLDLRSIRKQSKRGPSSECFWK 119
QY 121 YCI 123
DB 120 YCV 122
RESULT 10
AAU80120
ID AAU80120 standard; Protein; 122 AA.
AC AAU80120;
XX
XX
DT 07-QCT-2002 (first entry)
XX
DE Cow sensory epithelium neuropeptide-like receptor (SENR) protein.
XX
XX SENR; Sensory epithelium neuropeptide-like receptor; cow; fear;
KM attention deficit disorder; narcolepsy; anxiety; depression; insomnia;
KM schizophrenia; G protein-coupled; receptor.
XX
XX Bos taurus.
OS
XX
XX W0200214513-A1.
PN
XX
PD 21-FEB-2002.
XX
XX 10-AUG-2001; 2001WO-JP06899.
PF
XX 10-AUG-2000; 2000JP-0247968.
PR
XX
XX (TAKE) TAKEDA CHEM IND LTD.
PA
XX Matsumoto Y, Watanabe T, Takahashi H, Mori M;
PI
XX WPI; 2002-329576/36.
DR
XX
XX Polypeptide GPR12 with ligand activity to sensor epithelium
PT neuropeptide-like receptor, useful e.g. in treating attention deficit
PT disorder or narcolepsy, or for screening drug candidates for these
PT indications and for anxiety
XX

PS Claim 6; Page 276; 290pp; Japanese.
XX
XX This invention relates to an anti-attention deficit disorder or anti-
CC narcolepsy agent containing a polypeptide with a sequence identical or
CC substantially similar to a fully defined 12 amino acid sequence given in
CC the specification, and its amide, ester or their salt. The peptides
CC have ligand activity to sensory epithelium neuropeptide-like receptor
CC (SENR) protein. The invention also includes a method for diagnosing
CC attention deficit disorder, narcolepsy, anxiety, depression, insomnia,
CC schizophrenia or fear. The polypeptides of the invention, their
CC precursor proteins and their encoding DNAs are useful in treating
CC attention deficit disorder or narcolepsy, or for screening drug
CC candidates for these indications and for anxiety, depression, insomnia,
CC schizophrenia or fear. They are also useful for gene therapy. The
CC polypeptide is a G protein-coupled receptor protein, with ligand
CC activity to sensor epithelium neuropeptide-like receptor. The present
CC sequence represents the cow sensory endothelium neuropeptide-like
CC receptor protein of the invention.
XX
SQ Sequence 122 AA;
Query Match 48.8%; Score 312.5; DB 23; Length 122;
Best Local Similarity 52.8%; Pred. No. 2.7e-26;
Matches 65; Conservative 16; Mismatches 41; Indels 1; Gaps 1;
QY 1 MDRVPCCLLFTGLNPLSLPYDTGERTLQPLVEDALRALLELERNALLQTLRQTM 60
DB 1 MYKLVSCLLFTGLSLNPLSLPYLDSRQSLQ-LAPEVRSRLDELERSLLQMLPEMS 59
QY 61 GTFAGSPGEAGSTETPPRGSMRKAFAGQNSNTVLSRLARTRKQHKOHGAAPCFWK 120
DB 60 GAGTGGRLNTDPTITNIFYPRGMRRKAFSGQDPKFLSLDLRSIRKQSKRGPSSECFWK 119
QY 121 YCI 123
DB 120 YCV 122
RESULT 11
AAU93639
ID AAU93639 standard; Protein; 124 AA.
AC AAU93639;
XX
XX
DT 25-SEP-2000 (first entry)
XX
XX Amino acid sequence of a human prepro-urotensin II (III) polypeptide.
DE
XX
XX Urotensin II; motor neuron; hypertensive; neurodegeneration;
KM spinal cord trauma; hemi-plegia; para-plegia;
KM amyotrophic lateral sclerosis; antihypertensive agent.
XX
XX Homo sapiens.
OS
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Peptide /note="signal peptide"
FT Peptide 21..110
FT /note="pro-segment of urotensin II"
FT Misc-difference 46 /note="encoded by GAC"
FT Misc-difference 47 /note="encoded by GTA"
FT Misc-difference 81 /note="encoded by ATT"
FT Peptide 114..124 /note="urotensin II"
FT
XX
XX W0200031265-A1.
PN
XX 02-JUN-2000.
PD
XX
XX 26-NOV-1999; 99WO-FR02941.

XX 26-NOV-1998; 98FR-0014914.
 XX (INRM) INST NAT SANTE & RECH MEDICALE.
 PA Beauvillain J, Coulouarn Y, Jegou S, Lihmann I, Vaudry H;
 XX WPI: 2000-400075/34.
 DR N-PSDB; AAA46698.
 XX New mammalian urotensin II polypeptide, useful for treating
 PT neurodegeneration and spinal cord injury -
 XX Claim 2; Fig 2; 42pp; French.
 PS The present sequence represents a human prepro-urotensin II polypeptide.
 CC In mammals, urotensin II promotes survival and regeneration of motor
 CC neurons, and also has a hypertensive effect. The urotensin II
 CC polypeptides and polynucleotides are useful for treating
 CC neurodegeneration and trauma of the spinal cord (e.g. hemi-plegia,
 CC para-plegia or amyotrophic lateral sclerosis). The polypeptides
 CC are also used to screen for specific inhibitors, i.e. potential
 CC antihypertensive agents.
 XX Sequence 124 AA:
 SO
 Query Match 44.7%; Score 286.5; DB 21; Length 124;
 Best Local Similarity 49.6%; Pred. No. 1.9e-23;
 Matches 62; Conservative 19; Mismatches 41; Indels 3; Gaps 2;
 QY 1 MDRVPCCLFIFGLNPLSLPTDTGERTLPVLEEDLRALAELEERALLQTLRQTM 60
 DB 1 MYKLASCCLEIFGLNPLSLPLDSREISFOLSAPHEDRALPEELERASLLQILEMIL 60
 QY 61 GTEAGSPGAGSTETPTPRGSMRK--AFAGONSNTVLSSRLARTKOKHGAPECF 118
 DB 61 GAERGLDLRKADSTNINFRGNLRKQDFSGQDPNILLSHLARIMKPKYKR-ETPDCE 119
 QY 119 WKYCI 123
 DB 120 WKYCV 124
 Db
 RESULT 12
 AAY87319
 ID AAY87319 standard; protein: 124 AA.
 XX
 AC AAY87319;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE Human signal peptide containing protein HSP-96 SEQ ID NO:96.
 XX
 KW Human: signal peptide-containing protein; HSP; diagnosis; cancer;
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
 KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;
 KW antistimatic; gene therapy; cell proliferation; neurological disorder;
 KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX
 OS Homo sapiens.
 XX
 PN WO200000610-A2.
 XX
 PD 06-JAN-2000.
 XX
 PF 25-JUN-1999; 99WO-US14484.
 XX
 PR 26-JUN-1998; 98US-0090762.
 PR 31-JUL-1998; 98US-0094983.

PR 01-OCT-1998; 98US-0102686.
 PR 11-DEC-1998; 98US-0112129.
 XX
 XX (INCY-) INCYTE PHARM INC.
 PA Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom LE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI: 2000-160673/14.
 DR N-PSDB; AA298204.
 XX
 PT New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and
 PT cardiovascular disease -
 XX Claim 1; Page 221-222; 327pp; English.
 PS
 CC AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antistimatic activities, and can
 CC be used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense,
 CC triplex-forming or ribozyme therapeutics, for detecting related sequences
 CC or genetic variations, and for chromosomal mapping. HSP are also used to
 CC raise specific antibodies (Ab) and to screen for agonists and
 CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
 CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
 CC antagonists, in competitive drug screens, and for purification of HSP
 CC from natural sources.
 XX
 SO Sequence 124 AA;
 Query Match 44.7%; Score 286.5; DB 21; Length 124;
 Best Local Similarity 49.6%; Pred. No. 1.9e-23;
 Matches 62; Conservative 19; Mismatches 41; Indels 3; Gaps 2;
 QY 1 MDRVPCCLFIFGLNPLSLPTDTGERTLPVLEEDLRALAELEERALLQTLRQTM 60
 DB 1 MYKLASCCLEIFGLNPLSLPLDSREISFOLSAPHEDRALPEELERASLLQILEMIL 60
 QY 61 GTEAGSPGAGSTETPTPRGSMRK--AFAGONSNTVLSSRLARTKOKHGAPECF 118
 DB 61 GAERGLDLRKADSTNINFRGNLRKQDFSGQDPNILLSHLARIMKPKYKR-ETPDCE 119
 QY 119 WKYCI 123
 DB 120 WKYCV 124
 Db
 RESULT 13
 AAY66707
 ID AAY66707 standard; protein: 124 AA.
 XX
 AC AAY66707;
 XX
 DT 05-APR-2000 (first entry)
 XX
 DE Membrane-bound protein PRO1068.
 XX
 PR Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor Immunoadhesin; gene mapping.
XX
OS Homo sapiens.
XX WO963088-A2.
XX
PD 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088326.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088217.
PR 05-JUN-1998; 98US-0088212.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0088909.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089949.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090425.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.

PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090680.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090697.
PR 26-JUN-1998; 98US-0090698.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091489.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096766.
PR 17-AUG-1998; 98US-0096768.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097986.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-0100634.
PR 12-JAN-1999; 99US-0115565.


```

Oy      1 MDRAVECCCLFLGLNPLLSLVDPTDGTERTQLPVLLEDAALALEELERMAALLQTLRQTM 60
        1 : :: ||||| : |||||:: : : : | | | | | | | | | | : : :
Db       1 MYKLSACCLLFITGFLNPILLSLPDLDSREISFOLSAFHEDARTLPBELFRASLLQILPEWL 60
Oy      61 GTFACESPGEAGPSYTFETPRGCSMKR--AFAGONSNTVLSRLLAFTRKOKHOGAAPECF 118
Db      61 GAERKDILRKADSSININPNRGNLKKPFODFSQDPNILLSHLLARIMWKPKKR-ETPDCE 119
Oy      119 WKYCt 123
        11111:
Db      120 WKYCV 124
        .

RESULT 15
AAB65230
ID      AAB65230 standard; Protein: 124 AA.
XX
AC      AAB65230;
XX
DT      02-APR-2001 (first entry)
XX
DE      Human PRO1068 (UNQ525) protein sequence SEQ ID NO:266.
XX
KW      Human; secreted and transmembrane protein; pro; cytosstatic;
KW      cell death; cancer; Chromosomal mapping; gene mapping; tissue typing;
KW      diagnostic assay.
XX
OS      Homo sapiens.
XX
MN      WO200073454-A1.
XX
PD      07-DEC-2000
XX
PE      30-MAR-2000; 2000WO-US08439.
XX
PR      02-JUN-1999; 99WO-US12252.
PR      23-JUN-1999; 99US-O141037.
PR      07-JUL-1999; 99US-O143048.
PR      20-JUL-1999; 99US-O144758.
PR      26-JUL-1999; 99US-O145698.
PR      28-JUL-1999; 99US-O146222.
PR      17-AUG-1999; 99US-O149396.
PR      15-SEP-1999; 99WO-US21090.
PR      15-SEP-1999; 99WO-US21547.
PR      08-OCT-1999; 99US-O158663.
PR      30-NOV-1999; 99WO-US28313.
PR      01-DEC-1999; 99WO-US28301.
PR      16-DEC-1999; 99WO-US30095.
PR      20-DEC-1999; 99WO-US30911.
PR      05-JAN-2000; 2000WO-US00219.
PR      06-JAN-2000; 2000WO-US00376.
PR      11-FEB-2000; 2000WO-US03565.
PR      18-FEB-2000; 2000WO-US04341.
PR      22-FEB-2000; 2000WO-US04414.
PR      24-FEB-2000; 2000WO-US04914.
PR      24-FEB-2000; 2000WO-US05004.
PR      02-MAR-2000; 2000WO-US05841.
PR      15-MAR-2000; 2000WO-US06884.
PR      20-MAR-2000; 2000WO-US07377.
XX
PA      (GENETH ) GENENTECH INC.
XX
PI      Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI      Ferrara N, Fong S, Geber H, Gerlitsen ME, Goddard A, Godowski PJ
PI      Grimaldi CJ, Guney AL, Klavain IJ, Napier MA, Pan J, Paoni NF,
PI      Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WL;
PI      Zhang Z;
XX
DR      MPI, 2001-032160/04.
XX      N-P5DB; AAF44193.
XX
PT      PRO polynucleotides used to produce polypeptides used to target

```

bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -

Claim 12; Fig 184; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomes and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAT44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Query Match	Similarity	43.9%	Score	281.5	DB	22	Length	124	
Best Local	Similarity	48.8%	Pred.	No.6.7e-23					
Matches	61:	Conservative	19;	Mismatches	44;	Indels	3;	Gaps	2
Oy	1	MDRVPCCLLFTGLINPLSLPVTDTGERTKLDPVLEEDALPALLEEELSMALLQTLRQM	60						
	:	: : : : : : : : : : : : : : :							
Dd	1	MYKLSGCCLLFTGFLNPLSLPLDLSRLSPDLSRSLSPDSAPHDEARLTPELEERASILLQLPEWL	60						
Oy	61	GTEAGESPGCEAGSPTETPTPRGSMRK--AFAGCONSNTVLISRLLAATRKQKHGAAPCECF	118						
	:	: : : : : : : : : : : : : : :							
Dd	61	GAERGDIILKKADSSNIENFPRGNLRKFQSGODPENILLSHLARIIMKYKKR-ETPDGF	119						
Oy	119	WKYCI	123						
	:	: : : : :							
Dd	120	WKYCV	124						

Search completed: March 10, 2003, 17:38:45
Job time : 30.9189 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:37:08 ; Search time 11.3027 Seconds
(without alignments)
320.191 Million cell updates/sec

Title: US-09-831-907A-33

Perfect score: 641

Sequence: 1 MDRVPCCLIFGLNPLLS.....TRKHQKGAPECFWKYCI 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Issued_Patents_AA:*

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6: /cgn2_6/ptodata/2/1aa/Dackfilest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	201.5	31.4	139	US-09-027-381-2	Sequence 2, Appl1
2	201.5	31.4	139	US-09-477-071-2	Sequence 2, Appl1
3	195.5	30.5	103	US-09-027-381-4	Sequence 4, Appl1
4	195.5	30.5	103	US-09-477-071-4	Sequence 4, Appl1
5	76	11.9	605	US-08-472-666-1	Sequence 1, Appl1
6	76	11.9	605	PCT-US96-07615-1	Sequence 1, Appl1
7	75	11.7	966	US-08-571-758-2	Sequence 2, Appl1
8	75	11.7	966	US-08-909-984-2	Sequence 2, Appl1
9	75	11.7	966	US-08-909-984-2	Sequence 2, Appl1
10	73.5	11.5	1637	US-09-718-692-2	Sequence 2, Appl1
11	73.5	11.5	1637	US-09-718-852-2	Sequence 2, Appl1
12	73.5	11.5	1637	US-09-118-815-2	Sequence 2, Appl1
13	72	11.2	6095	US-09-144-085-2	Sequence 2, Appl1
14	69.5	10.8	264	US-08-713-556F-42	Sequence 42, Appl1
15	68.5	10.7	436	US-08-958-642-4	Sequence 4, Appl1
16	68.5	10.7	436	US-08-778-394-2	Sequence 2, Appl1
17	68.5	10.7	436	US-08-778-423A-4	Sequence 4, Appl1
18	66.5	10.4	291	PCT-US93-05000-6	Sequence 6, Appl1
19	66.5	10.4	292	US-08-464-517-23	Sequence 23, Appl1
20	66.5	10.4	292	US-08-246-361A-6	Sequence 6, Appl1
21	66.5	10.4	292	US-08-246-361A-23	Sequence 23, Appl1
22	66.5	10.4	292	US-08-463-772-23	Sequence 23, Appl1
23	66.5	10.4	292	PCT-US93-05000-23	Sequence 23, Appl1
24	66.5	10.4	1244	US-08-938-291A-5	Sequence 5, Appl1
25	66	10.3	271	US-09-414-436-1	Sequence 1, Appl1
26	66	10.3	546	US-08-935-855-20	Sequence 20, Appl1
27	65.5	10.2	297	US-09-006-535-4	Sequence 4, Appl1

28	65.5	10.2	1093	PCT-US93-03077-1	Sequence 1, Appl1
29	64.5	10.1	560	US-08-592-500-2	Sequence 2, Appl1
30	64.5	10.1	560	US-08-195-006-2	Sequence 2, Appl1
31	64.5	10.1	560	US-09-063-950-4	Sequence 4, Appl1
32	64.5	10.1	560	PCT-US94-07644A-2	Sequence 2, Appl1
33	64	10.0	763	US-08-742-753-4	Sequence 4, Appl1
34	64	10.0	1976	US-09-024-020B-9	Sequence 9, Appl1
35	64	10.0	1976	US-09-425-043-9	Sequence 9, Appl1
36	63	9.8	468	US-08-459-287-3	Sequence 3, Appl1
37	63	9.8	1978	US-09-024-020B-3	Sequence 3, Appl1
38	63	9.8	1978	US-09-425-043-3	Sequence 3, Appl1
39	63	9.8	1988	US-09-024-020B-4	Sequence 4, Appl1
40	63	9.8	1988	US-09-425-043-4	Sequence 4, Appl1
41	62.5	9.8	501	US-08-969-630-4	Sequence 4, Appl1
42	62.5	9.8	501	US-08-906-791-2	Sequence 2, Appl1
43	62.5	9.8	514	US-08-974-549A-605	Sequence 605, App
44	62.5	9.8	830	US-09-562-737-39	Sequence 39, Appl1
45	62	9.7	247	US-09-157-864-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-027-381-2
Sequence 2, Application US/09027381
Patent No. 6075137
GENERAL INFORMATION:
APPLICANT: CULP, JEFFREY
APPLICANT: MCNULTY, DEAN
APPLICANT: ELLIS, CATHERINE
TITLE OF INVENTION: HUMAN UROGENSIN II
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,381
FILING DATE: 20-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/072,383
FILING DATE: 09-JAN-1998
APPLICATION NUMBER: GP-70366-1P
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 139 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-027-381-2
Query Match 31.4%; Score 201.5; DB 3; Length 139;
Best Local Similarity 43.2%; Pred. No. 2.3e-16;

QY 75 TETPTPGSMRK - - AFAGQNSNTVLSRLARTRKQHKQGAPECFWKYCL 123

Db 54 TINFNPGNLKRFODESGODENILSLHLLATKMKPYKKR-ETPPGFMKYCV 103

RESULT 5

US-08-472-666-1

Sequence 1, Application US/08472666

Patent No. 5821048

GENERAL INFORMATION:

APPLICANT: Howley, Peter M.

APPLICANT: Benson, John D.

APPLICANT: Yasugli, Toshiharu

APPLICANT: Sakai, Hiroyuki

TITLE OF INVENTION: METHOD AND KIT FOR DIAGNOSING

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ann-Louise Kerner, Ph.D.

ADDRESS: Lappin & Kusmer

STREET: 200 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 01209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,666

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: McDaniel, Patricia A.

REGISTRATION NUMBER: 33,194

REFERENCE/DOCKET NUMBER: HAZ-010

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-330-1300

TELEFAX: 617-330-1311

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 605 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORGANISM: Bovine papillomavirus E1

STRAIN: BPV-1

US-08-472-666-1

Query Match 11.9%; Score 76; DB 2; Length 605;

Best Local Similarity 28.9%; Pred. No. 1.4;

Matches 24; Conservative 16; Mismatches 33; Indels 10; Gaps 3;

Db 35 VLEEDALRALEELERMA-----LLOTLRQTMGTGEGSPGAGSTPTPTPR---GSMRKA 87

Db 59 VFQGNHLEVFQALEKKEGEQIILNKKRVLGSSONSSGSEA---SETPVRRKSGAKRRL 115

Db 88 FAGONSNTVLSRLAARTKROKQ 110

Db 116 FAENEANRVLTPLQVOGEGEGRQ 138

RESULT 6

PCT-US96-07615-1

Sequence 1, Application PC/TUS9607615

GENERAL INFORMATION:

APPLICANT: PRESIDENT AND FELLOWS OF HARVARD COLLEGE

TITLE OF INVENTION: METHODS, KITS, AND COMPOSITIONS FOR DIAGNOSING

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lappin & Kusmer

STREET: 200 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 01209

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/07615

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kerner, Ann-Louise

REGISTRATION NUMBER: 33,523

REFERENCE/DOCKET NUMBER: HAZ-010PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-330-1300

TELEFAX: 617-330-1311

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 605 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

ORGANISM: Bovine papillomavirus E1

STRAIN: BPV-1

PCT-US96-07615-1

Query Match 11.9%; Score 76; DB 5; Length 605;

Best Local Similarity 28.9%; Pred. No. 1.4;

Matches 24; Conservative 16; Mismatches 33; Indels 10; Gaps 3;

Db 35 VLEEDALRALEELERMA-----LLOTLRQTMGTGEGSPGAGSTPTPTPR---GSMRKA 87

Db 59 VFQGNHLEVFQALEKKEGEQIILNKKRVLGSSONSSGSEA---SETPVRRKSGAKRRL 115

Db 88 FAGONSNTVLSRLAARTKROKQ 110

Db 116 FAENEANRVLTPLQVOGEGEGRQ 138

RESULT 7

US-08-571-758-2

Sequence 2, Application US/08571758

Patent No. 5700675

GENERAL INFORMATION:

APPLICANT: Rubin, Gerry M.

APPLICANT: Therrien, Marc

APPLICANT: Chang, Henry C.

APPLICANT: Karim, Felix D.

TITLE OF INVENTION: A No. 5700675e1 Protein Kinase Required for Ras

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/571,758

	Query Match	11.7%	Score 75:	DB I:	Length 966;
	Beat Local Similarity	30.4%;	Pred.	No. 3.4;	
	Matches	35:	Conservative	13:	Mismatches 45; Indels 22; Gaps 7.
QY	8	CLFLGILNPLLSVPVDTGERTLDPVLVEEDALALAELEBMA-LLOPLRQTM-STEAG	65		
DQ	121	CLARITLTLEQSURL-----SDEETROL-LADSSQSEEEELRLPTRAOMQLKRCMESLEG	175		
QY	66	ESPEACG-----STPTPT--PRGSMKAFAGONSNTVLSRLARTRKONQH	112		
DB	176	TAAANNDEQIMHDSWDRPTHNRGSVCNIGLCNNST-----ASPRHNHHQH	223		

RESULT 8
 US-08-909-984A-2
 Sequence 2, Application US/08909984A
 Patent No. 5747275
 GENERAL INFORMATION:
 APPLICANT: Rudin, Gerry M.
 APPLICANT: Therrien, Marc
 APPLICANT: Chang, Henry C.
 APPLICANT: Karim, Felix D.
 APPLICANT: Massarman, David A.
 TITLE OF INVENTION: A No. 5747275e1 Protein Kinase Required for Ras
 TITLE OF INVENTION: Signal Transduction
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 BUSH STREET, SUITE 3200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/909,984A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OSMAN, RICHARD A.
 REGISTRATION NUMBER: 36,627
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 343-4341
 TELEFAX: (415) 343-4342
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 966 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant

[illegible]

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US-08-909-983-2
: Sequence 2, Application US/08909983
: Patent No. 5747288
: GENERAL INFORMATION:
: APPLICANT: Rubin, Gerry M.
: APPLICANT: Therrien, Marc
: APPLICANT: Chang, Henry C.
: APPLICANT: Karim, Felix D.
: APPLICANT: Wasserman, David A.
: TITLE OF INVENTION: A No. 5747288el Protein Kinase Required for Ras
: TITLE OF INVENTION: Signal Transduction
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
: STREET: 268 BUSH STREET, SUITE 3200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: USA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/909,983
: FILING DATE: 12-JUN-1997
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/571,758
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: OSMAN, RICHARD A
: REGISTRATION NUMBER: 36,627
: REFERENCE/DOCKET NUMBER: B96-010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 343-4341
: TELEFAX: (415) 343-4342
: INFORMATION FOR SEQ. ID NO. 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 966 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: US-08-909-983-2

Query Match 11.7%; Score 75; DB 1; Length 966;
Best Local Similarity 30.4%; Pred. No. 3.4;
Matches 35; Conservative 13; Mismatches 45; Indels 22; Gaps 7

QY 8 CULFLGILNPLSLPYDTGERTLQPLVLEEDALRALAELEERMA-LLQTLRQTM-STEAG 65
DB 121 CLARLTTLRQSLURL----SDEELRLQ-LADSPQGRREELRLTRAMQNLKRCMESLESG 175
QY 66 ESPGEGAP-----STETPT--PRGSMKRAFAQONSNTVLSRLAARTTKRKHQHG 112

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Db 176 TAASNDPQMHWSWDRPHIRGSGVNLGNST-----ASPRHHQHGS 223

RESULT 10

US-09-718-692-2

; Sequence 2, Application US/09718692
; Patent No. 6383796
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6383796e1 motor proteins and methods for
; FILE REFERENCE: 1052
; CURRENT APPLICATION NUMBER: US/09/718,692
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1637
; TYPE: PRT
; ORGANISM: Human
US-09-718-692-2

Query Match 11.5%; Score 73.5; DB 4; Length 1637;
Best Local Similarity 25.0%; Pred. No. 10;

Matches 28; Conservative 27; Mismatches 46; Indels 11; Gaps 4;

Qy 14 LNPPLSLPVTDTGERTLQPLVEEDALRALEE-----LERMALLQTLRQTMGTAGEESP 68

Db 455 LMSQANLLAKAGDGNFALIGNIYRIEIEELTKLLESEAMNESLRSLRSASARSP 514

Qy 69 GEAGSTETPTPRGSMRKAFAGONSNTVLSRL--LARTRKQK-KQHGAPF 116

Db 515 YSLGASPAAPAFGGS--PASSMEDASEVIRAKODLERLKKKEVQRKRSPE 564

RESULT 11

US-09-718-852-2

; Sequence 2, Application US/09718852
; Patent No. 6426193
; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6426193e1 motor proteins and methods for
; FILE REFERENCE: 1052
; CURRENT APPLICATION NUMBER: US/09/718,852
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1637
; TYPE: PRT
; ORGANISM: Human
US-09-718-852-2

Query Match 11.5%; Score 73.5; DB 4; Length 1637;
Best Local Similarity 25.0%; Pred. No. 10;

Matches 28; Conservative 27; Mismatches 46; Indels 11; Gaps 4;

Qy 14 LNPPLSLPVTDTGERTLQPLVEEDALRALEE-----LERMALLQTLRQTMGTAGEESP 68

Db 455 LMSQANLLAKAGDGNFALIGNIYRIEIEELTKLLESEAMNESLRSLRSASARSP 514

Qy 69 GEAGSTETPTPRGSMRKAFAGONSNTVLSRL--LARTRKQK-KQHGAPF 116

Db 515 YSLGASPAAPAFGGS--PASSMEDASEVIRAKODLERLKKKEVQRKRSPE 564

RESULT 12

US-09-718-815-2

; Sequence 2, Application US/09718815

; Patent No. 6455293

; GENERAL INFORMATION:
; APPLICANT: Beraud, Christophe
; APPLICANT: Freedman, Richard
; TITLE OF INVENTION: No. 6455293e1 motor proteins and methods for
; FILE REFERENCE: 1052
; CURRENT APPLICATION NUMBER: US/09/718,815
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1637
; TYPE: PRT
; ORGANISM: Human
US-09-718-815-2

Query Match 11.5%; Score 73.5; DB 4; Length 1637;
Best Local Similarity 25.0%; Pred. No. 10;

Matches 28; Conservative 27; Mismatches 46; Indels 11; Gaps 4;

Qy 14 LNPPLSLPVTDTGERTLQPLVEEDALRALEE-----LERMALLQTLRQTMGTAGEESP 68

Db 455 LMSQANLLAKAGDGNFALIGNIYRIEIEELTKLLESEAMNESLRSLRSASARSP 514

Qy 69 GEAGSTETPTPRGSMRKAFAGONSNTVLSRL--LARTRKQK-KQHGAPF 116

Db 515 YSLGASPAAPAFGGS--PASSMEDASEVIRAKODLERLKKKEVQRKRSPE 564

RESULT 13

US-09-144-085-2

; Sequence 2, Application US/09144085
; Patent No. 6280999
; GENERAL INFORMATION:
; APPLICANT: Gustafsson, Claes
; APPLICANT: Ashley, Gary
; APPLICANT: Julien, Bryan
; APPLICANT: Ziermann, Rainer
; TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
; FILE REFERENCE: 30062-20020.20
; CURRENT APPLICATION NUMBER: US/09/144,085
; CURRENT FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: 09/010,809
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6095
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-144-085-2

Query Match 11.2%; Score 72; DB 4; Length 6095;
Best Local Similarity 24.2%; Pred. No. 91;

Matches 39; Conservative 18; Mismatches 50; Indels 54; Gaps 7;

Qy 10 LFTGLNPLSLPVTDTGERTLQPLVEEDALRALEERW-ALLQTLRQTMGTAGEESP 68

Db 1679 LFRALLRSLRKASSATRRDASAL-----RETLSPALPATERLNLVLRGEVAAVAGIQR 1734

Qy 69 GEAGPS-----TET-----PTPRG-----SMRKAFAG 90

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Qy 91 QNSNTVLSRLARTRKQK-----KQHG--AAPECFWK 120

Db 1795 LQYKARARVRRAGKDEPIAIVSMACRLPGVATPDQYWR 1835

RESULT 14

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:38:48 ; Search time 9.64054 Seconds
(without alignments)
538.033 Million cell updates/sec

Title: US-09-831-907A-33

Perfect score: 641
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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14: /cgn2-6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	293	45.7	125	10	US-09-854-105-2
2	281.5	43.9	124	9	US-09-992-598-266
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4	281.5	43.9	124	9	US-09-989-734-266
5	281.5	43.9	124	9	US-09-990-444-266
6	281.5	43.9	124	9	US-09-989-730-266
7	281.5	43.9	124	9	US-09-990-436-266
8	281.5	43.9	124	9	US-09-993-687-266
9	281.5	43.9	124	9	US-09-993-687-266
10	281.5	43.9	124	9	US-09-989-734-266
11	281.5	43.9	124	9	US-09-997-653-266
12	281.5	43.9	124	9	US-09-993-667-266
13	281.5	43.9	124	9	US-09-990-438-266
14	281.5	43.9	124	9	US-09-990-562-266
15	281.5	43.9	124	9	US-09-997-666-266
16	281.5	43.9	124	9	US-09-990-711-266
17	281.5	43.9	124	9	US-09-989-726-266
18	281.5	43.9	124	9	US-09-989-726-266
19	281.5	43.9	124	10	US-09-989-722-266

20	281.5	43.9	124	10	US-09-989-723-266	Sequence 266, App
21	281.5	43.9	124	10	US-09-989-279-266	Sequence 266, App
22	281.5	43.9	124	10	US-09-989-727-266	Sequence 266, App
23	281.5	43.9	124	10	US-09-989-731-266	Sequence 266, App
24	281.5	43.9	124	10	US-09-989-732-266	Sequence 266, App
25	281.5	43.9	124	10	US-09-991-073-266	Sequence 266, App
26	281.5	43.9	124	10	US-09-990-442-266	Sequence 266, App
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28	281.5	43.9	124	10	US-09-993-604-266	Sequence 266, App
29	281.5	43.9	124	10	US-09-990-456-266	Sequence 266, App
30	281.5	43.9	124	10	US-09-989-721-266	Sequence 266, App
31	89	13.9	2249	9	US-09-866-557A-4	Sequence 4, App11
32	85.5	13.3	256	10	US-09-867-550-684	Sequence 684, App
33	73	11.4	596	10	US-09-797-039-8	Sequence 8, App11
34	71	11.1	208	9	US-09-738-626-6261	Sequence 6261, App
35	70.5	11.0	315	10	US-09-925-301-1053	Sequence 1053, App
36	70	10.9	1478	10	US-09-801-368-52	Sequence 52, App1
37	66	10.3	491	9	US-10-114-893-69	Sequence 69, App1
38	65.5	10.2	434	10	US-09-815-242-4987	Sequence 4987, App
39	65.5	10.2	448	10	US-09-815-242-10651	Sequence 10651, App
40	65.5	10.2	1033	9	US-09-823-356-9	Sequence 9, App11
41	65.5	10.2	950	10	US-09-820-843A-75	Sequence 75, App1
42	65	10.1	178	9	US-09-764-868-792	Sequence 792, App
43	64.5	10.1	560	10	US-09-782-980-61	Sequence 61, App1
44	64.5	10.1	568	9	US-10-173-519-2	Sequence 2, App11
45	64	10.0	238	9	US-09-738-626-6690	Sequence 6690, App

ALIGNMENTS

RESULT 1
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Sequence 2, Application US/09854105
Patent No. US20020058323A1
GENERAL INFORMATION:
APPLICANT: Elshoutbagy, Nabil
APPLICANT: Shabon, Usman
TITLE OF INVENTION: MONKEY UROTENSIN II
FILE REFERENCE: GP-70694
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 60/203,470
PRIOR FILING DATE: 2000-05-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 125
TYPE: PRT
ORGANISM: MACACA FASCICULARIS
US-09-854-105-2

Query Match 45.7%, Score 293; DB 10: Length 125;
Best Local Similarity 50.8%, Pred. No. 1.9e-23;
Matches 64; Conservative 19; Mismatches 39; Indels 4; Gaps 3;

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DB 61 LGAEKRGSLRAKADSTINFNKRLKRFQDFSGDDPLLSSHLLARLRKPYKKR-ETPDC 119
QY 118 FMKYCI 123
DB 120 FMKYCV 125

RESULT 2
US-09-992-598-266
Sequence 266, Application US/09992598
Patent No. US20020160384A1

GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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APPLICANT: Gerber, Hanspeter
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
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Best Local Similarity 48.8%; Pred. No. 36-22;

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DB 120 WKYCV 124

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RESULT 3
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; Sequence 266, Application US/09989293A

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; Patent No. US20020177164A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Napier, Mary A.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 43.9% Score 281.5; DB 9; Length 124;
Best Local Similarity 48.8%; Pred. No. 3e-22;
Matches 61; Conservative 19; Mismatches 42; Indels 3; Gaps 2;

QY 1 MDRVPCCLFTGLNPLSLPVTGERTQLPYLEEDALALELERMALLOTLRQTM 60
DB 1 MYKLASCCLEFTGLPLSLPLDLSREISFOLSAPHEDARLTPEELERASLIQILPEML 60
QY 61 GTEAGESPEAGSTETTPRGSMRK--AFAGONSMTVLSRLIARTROHKONGAPECF 118
DB 61 GAEKGDILKADSTNIENPRGNLKRKFQFSGODPNILSLHLARIWKYKKR-ETPDCE 119
QY 119 WKYCI 123
DB 120 WKYCV 124

RESULT 4
US-09-989-735-266

Sequence 266, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23

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3	PRIOR FILING DATE: 1998-06-24
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9	PRIOR APPLICATION NUMBER: 60/090435
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11	PRIOR FILING DATE: 1998-06-24
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13	PRIOR APPLICATION NUMBER: 60/090444
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21	PRIOR APPLICATION NUMBER: 60/090472
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85	PRIOR APPLICATION NUMBER: 60/091519
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89	PRIOR APPLICATION NUMBER: 60/091626
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91	PRIOR FILING DATE: 1998-07-02
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93	PRIOR APPLICATION NUMBER: 60/091633
94	
95	PRIOR FILING DATE: 1998-07-02
96	
97	PRIOR APPLICATION NUMBER: 60/091978
98	
99	PRIOR FILING DATE: 1998-07-07
100	
101	PRIOR APPLICATION NUMBER: 60/091982
102	
103	PRIOR FILING DATE: 1998-07-07
104	
105	PRIOR APPLICATION NUMBER: 60/092182
106	
107	PRIOR FILING DATE: 1998-07-09

Query Match	43.9%	Score 281.5	DB 9	Length 124
Best Local Similarity	48.8%	Pred. No. 3e-22	42	Gaps 2
Matches 61	Conservative 19	Mismatches 42	Indels 3	Gaps 2

QY	1	MDRVPCCLLEFTGLINPLSLPEVTDGTERTQLQPVLEEDALRALELEERMAALLQTLRQTM	60
		:: :: :: :: :	
Db	1	MYKLASCCLLEFTGFENPLSLPLDLSREISFLSPAHNEARLTPLELEFASVLIQIIPML	60
QY	61	GTEAGESEGEAGPSTETPTPGCSMKR--AFAQNSNTYVSRLLARTPKOHKOGAPCECF	118
		:: :: :: :: ::	
Db	61	GAERDILRKADSNININPRGNLKKFQFQSQDDNILSLHLARLWKKYKKR-ETPPDGF	119
QY	119	WKYCI	123
		:	
Db	120	WKYCV	124

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US-09-990-444-266
; Sequence 266, Application US/09990444
; Publication No. US20020193300A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gutney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC19
; CURRENT APPLICATION NUMBER: US/09/990.444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/04987
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
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; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
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; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/088033	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326	PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167	PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217	PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202	PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212	PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655	PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088821	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826	PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876	PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105	PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514	PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089599	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653	PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908	PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952	PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254	PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349	PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355	PRIOR FILING DATE: 1998-06-23

QY	61	GTAAAGSPGAGSTETPTPRGSMKK--AFAGONSNTVLSRLATRTKRONKHGAARPCF	118
Db	61	GAERGDILRKADSSNTINFNPRGNLKRKFDDFSQDPNILLSHLARIWKPKRK-ETPDCE	119
QY	119	WKYCI 123	
Db	120	WKYCV 124	

RESULT 6
US-09-989-730-266
Sequence 266, Application US/09989730
Publication NO. US20020197674A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: AGIS Encoding Line Same
FILE REFERENCE: P2730PIC59
CURRENT APPLICATION NUMBER: US/09/989,730
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23

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 26 PRIOR FILING DATE: 1998-06-25
 27 PRIOR APPLICATION NUMBER: 60/090690
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 29 PRIOR APPLICATION NUMBER: 60/090694
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 33 PRIOR APPLICATION NUMBER: 60/090696
 34 PRIOR FILING DATE: 1998-06-25
 35 PRIOR APPLICATION NUMBER: 60/090862
 36 PRIOR FILING DATE: 1998-06-26
 37 PRIOR APPLICATION NUMBER: 60/090863
 38 PRIOR FILING DATE: 1998-06-26
 39 PRIOR APPLICATION NUMBER: 60/091360
 40 PRIOR FILING DATE: 1998-07-01
 41 PRIOR APPLICATION NUMBER: 60/091478
 42 PRIOR FILING DATE: 1998-07-02
 43 PRIOR APPLICATION NUMBER: 60/091544
 44 PRIOR FILING DATE: 1998-07-01
 45 PRIOR APPLICATION NUMBER: 60/091519
 46 PRIOR FILING DATE: 1998-07-02
 47 PRIOR APPLICATION NUMBER: 60/091626
 48 PRIOR FILING DATE: 1998-07-02
 49 PRIOR APPLICATION NUMBER: 60/091633
 50 PRIOR FILING DATE: 1998-07-02
 51 PRIOR APPLICATION NUMBER: 60/091978
 52 PRIOR FILING DATE: 1998-07-07
 53 PRIOR APPLICATION NUMBER: 60/091982
 54 PRIOR FILING DATE: 1998-07-07
 55 PRIOR APPLICATION NUMBER: 60/092182
 56 PRIOR FILING DATE: 1998-07-09

[illegible]

RESULT 7
US-09-990-436-266
Sequence 266, Application US/09990436
Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertslen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tunas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990.436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04

RESULT 8
: Sequence 266, Application US/09991181
: Publication No. US20020197615A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Guiney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C53
: CURRENT APPLICATION NUMBER: US/09/991,181
: PRIOR FILING DATE: 2001-11-16
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
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: PRIOR APPLICATION NUMBER: 60/084600
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: PRIOR APPLICATION NUMBER: 60/087609
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: PRIOR APPLICATION NUMBER: 60/087759
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
: PRIOR APPLICATION NUMBER: 60/088021
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: PRIOR FILING DATE: 1998-06-18
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: PRIOR FILING DATE: 1998-06-22
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: PRIOR FILING DATE: 1998-06-22
: PRIOR APPLICATION NUMBER: 60/090254
: PRIOR FILING DATE: 1998-06-22

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PRIORITY APPLICATION NUMBER: 60/090349
PRIORITY FILING DATE: 1998-06-23
PRIORITY APPLICATION NUMBER: 60/090355
PRIORITY FILING DATE: 1998-06-23
PRIORITY APPLICATION NUMBER: 60/090429
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090431
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090435
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090444
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090445
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090472
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PRIORITY APPLICATION NUMBER: 60/090540
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090542
PRIORITY FILING DATE: 1998-06-24
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PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091633
PRIORITY FILING DATE: 1998-07-02
PRIORITY APPLICATION NUMBER: 60/091978
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/091982
PRIORITY FILING DATE: 1998-07-07
PRIORITY APPLICATION NUMBER: 60/092182
PRIORITY FILING DATE: 1998-07-09

Query Match 43.9%; Score 281.5; DB 9; Length 124;
Best Local Similarity 48.8%; Pred. NO. 3e-22;
Matches 61; Conservative 19; Mismatches 42; Indels 3; Gaps 2

QY 1 MDRVPCCLLFIGLNPPLSLPVTDTGERTIQLPVLEEDALRALBEERMAALLQTLRQTM 60
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DB 1 MYKLASCOLLFGFLNPPLSLPLDLSREISFOLSAVPHEDARLTPELERASLLQIDPEML 60

OY 61 GTEAGESEGEAGPSTETPTPGCSMKR--AFAGQNSNTVLSSRLARTKKOHKONGAAPDEF 118
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 61 GAEREDILRKADSSNIIEFPRGNLRKRFQDSODPNIILSHLLARIWKPKYKR-ETPDCF 119
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   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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Db      120 WKYCV 124

RESULT 9
US-09-993-687-266
: Sequence 266, Application US/09993687
: Publication No. US2002019819A1
GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kljavin, Ivar J.
: APPLICANT: Nepier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730PIC11
: CURRENT APPLICATION NUMBER: US/09/993,687
CURRENT FILING DATE: 2002-11-14
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
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: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
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: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088025
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: PRIOR FILING DATE: 1998-06-04
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: PRIOR FILING DATE: 1998-06-04

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PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-19
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PRIOR APPLICATION NUMBER: 60/090254

PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 43.9% Score 281.5; DB 9; Length 124;
Best Local Similarity 48.8% Pred. No. 3e-22;
Matches 61; Conservative 19; Mismatches 42; Indels 3; Gaps 2;

QY 1 MDRVPCCILFTGLNPLSLPVDTGERTQTLVLEEDALRALEBEERALLQTLQTM 60
Db 1 MYKLASCCLLFTGLNPLSLPLDSREISFOLSAPEHEDATPEELERASLQILPEML 60
QY 61 GTEAGESPGEAGSTETTPPGSMRK--AFAGONSNTVLSRLARTKQKHQHAABECF 118
Db 61 GAERGDILRKADSTNIFNPGNLRKFQDFSGODPNILSLHLARIMKPKKR-ETPDCF 119
QY 119 WKYCI 123

Db 120 WKYCV 124

RESULT 10

US-09-989-734-266

Sequence 266. Application us/09989734

PUBLICATION NO. US20030003531A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kijavlin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

FILE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C64

CURRENT APPLICATION NUMBER: US/09/989,734

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/076910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

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PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028

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;; PRIOR APPLICATION NUMBER: 60/090254
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 43.9%; Score 281.5; DB 9; Length 124;
Best Local Similarity 48.8%; Pred. No. 3e-22;
Matches 61; Conservative 19; Mismatches 42; Indels 3; Gaps 2;

OY 1 MDRVPECLIFIGLNLSPVDTGERTIQFVLEEDALRALAELEERALLQTLRQTM 60
Db 1 MYKLASCLLFTGFLNLSPVDTGERTIQFVLEEDALRALAELEERALLQTLRQTM 60
OY 61 GTEAGESPGEAGPSTETPPRGSMRK--AFAGONSNTVLSTLARTKQKHOGCADECF 118
Db 61 GAEGNDILRKADSTNTFNPRGNLRKFDPSGDDPNILSLHLARIRKPYKKR-ETPDCE 119

OY 119 WKYCI 123
Db 120 WKYCV 124

RESULT 11
US-09-997-653-266
; Sequence 266, Application US/09997653
; Publication No. US20030008297A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertlisen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kjaevlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC38
; CURRENT APPLICATION NUMBER: US/09/997,653
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 43.9%; Score 281.5; DB 9; Length 124;
Best Local Similarity 48.8%; Pred. No. 3e-22; Indels 3; Gaps 2;
Matches 61; Conservative 19; Mismatches 42;

OY 1 MDVFPCCLEFLGILNPLSTPYTDTGERTLOLPVLEEDALRALAELEENMALLQTLROT 60
I : : ||||| I ||||| I : : I : : || ||||| I : : I : :
DB 1 WKVLASCCLEFLGILNPLSTPYTDTGERTLOLPVLEEDALRALAELEENMALLQTLPE 60
I : : ||||| I ||||| I : : I : : || ||||| I : : I : :
OY 61 GTEAGESPEAGSTETPPRGSMRK--AFAGONSVTVLISRLIARTRKONKHGAAPBECF 118
I : : ||||| I ||||| I : : I : : || ||||| I : : I : :
DB 61 GAERGDIUKKADSTNIIFNDRGNLRKFFQDFSSGDDPITLLSHLARIWKPKR-ETPPDCF 119

QY 119 WKYC 123.
1111:
Db 120 WKYC 124

RESULT 12
US-09-993-667-266

Sequence 266, Application US/09993667
Publication No. US2003022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C4
CURRENT APPLICATION NUMBER: US/09/993,667
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PRIOR FILING DATE: 1997-06-16
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67	PRIOR APPLICATION NUMBER: 60/089801	68	PRIOR FILING DATE: 1998-06-18
69	PRIOR APPLICATION NUMBER: 60/089907	70	PRIOR FILING DATE: 1998-06-18
71	PRIOR APPLICATION NUMBER: 60/089908	72	PRIOR FILING DATE: 1998-06-18
73	PRIOR APPLICATION NUMBER: 60/089947	74	PRIOR FILING DATE: 1998-06-19
75	PRIOR APPLICATION NUMBER: 60/089948	76	PRIOR FILING DATE: 1998-06-19
77	PRIOR APPLICATION NUMBER: 60/089952	78	PRIOR FILING DATE: 1998-06-19
79	PRIOR APPLICATION NUMBER: 60/090246	80	PRIOR FILING DATE: 1998-06-19

Query Match	43.98	Score 281.5	DB 9	Length 124	
Best Local Similarity	48.88	Pred. No. 3e-22			
Matches 61	Conservative 19	Mismatches 42	Totals 3	Gaps 2	

Oy 1 MDVNPCCLLFLGLINPLLSLPTVDITGERTLOLPVEEDALRALREELSMALLQTLRQT 60
- :: ||||| | ||||| : : : || || ||||| : || : :
Db 1 MKRLASCCLLPFGFNLPLSLPLDLSREISFQLSAPHEDALRLPDETERASLIQLTPML 60
61 GTEDAGESPEGEACSTETPTTPEGSMRK--AFAGONSMTVLSSRLIAPT RKOHKOHGAAPCF 118

Db 61 GAERGDLRKADSTNIFNRGNLRKQDFSGODPNLLSHLLARIMKPYKKR-ETPDCF 119
QY 119 WKYCI 123
Db 120 WKYCV 124

RESULT 14
US-09-990-562-266
; Sequence 266, Application US/09990562
; Publication No. US20030027985A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bolstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertschen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C18
; CURRENT FILING DATE: US/09/990,562
; PRIOR APPLICATION NUMBER: 60/045787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR FILING DATE: 1998-06-03
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025

; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/089952
; PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: 60/090246
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PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
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PRIOR FILING DATE: 1998-06-23
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PRIOR FILING DATE: 1998-06-23
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PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
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PRIOR FILING DATE: 1998-06-26
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match
Best Local Similarity 43.98; Score 281.5; DB 9; Length 124;
Matches 61; Conservative 19; Mismatches 42; Indels 3; Gaps 2;

QY 1 MDRVPFCLLFGLNLLSLPYDTGERTLOFVLEEDLRALEELERNAILOTLRQTM 60
1 MYLASCLLFTGTGLNLLSLPLDSDREISFOJLAPHEADRLTFPEELERASLILOILEM 60

QY 61 GTEAGSGEAGPSTETPPRGSMRK--AFAGONSMTVLRLAPRKOHGGAPECF 118
Db 61 GAERGDIIRKADSDSTNIFNPRGNLRKFQFSDQENIILSHLARIMKPKR-ETPDF 119
QY 119 WKYCI 123
Db 120 WKYCV 124

RESULT 15
US-09-997-428-266
Sequence 266, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geriltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC44
CURRENT APPLICATION NUMBER: US/09/997,428
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/089947
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 43.9%; Score 281.5; DB 9; Length 124;

Best Local Similarity 48.8%; Pred. No. 3e-22; Indels 3; Gaps 2;

Matches 61; Conservative 19; Mismatches 42;

OY 1 MDKVPCCCLFGLNPLSLPTDGTGERTLOPLVEEDALRALALETERNALLOTLRQTM 60
DB 1 MYKLASCCLLFTGLNPLSLPLDLSREISFOLSAPREDAKRLTPEELERSLSLOIPEML 60

Tue Mar 11 10:10:36 2003

us-09-831-907a-33.rapb

Page 23

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Oy 61 GTEGSESGEGPSTETPTTPRGSMRK--AFAGONSNTVLSRLRLARTKQKHOGADEF 118
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 GAERKDIIRKADSTNIFNPRGNLTKRKPODESGDDPNILSLHLARITKPKRR-ETPDCE 119
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 119 WKYCI 123
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 WKYCV 124
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: March 10, 2003, 17:48:54
Job time : 10.6405 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2003, 17:36:23 ; Search time 13.2973 Seconds
(without alignments)
889.243 Million cell updates/sec

Title: US-09-831-907A-33

Perfect score: 641

Sequence: 1 MDRVPECCILFLGLNPLLS.....TRKHKGGADECEWYCI 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	115	17.9	125	2	I50499	urotensin II-gamma
2	101.5	15.8	125	2	I50498	urotensin II-alpha
3	79	12.3	523	2	S42727	translation initia
4	76.5	11.9	391	2	T17239	hypothetical prote
5	76	11.9	605	1	W1WLEB	hypothetical prote
6	75.5	11.8	111	2	H72526	hypothetical prote
7	75.5	11.8	663	2	A91048	probable 2-compone
8	75.5	11.8	663	2	B65025	hypothetical prote
9	73.5	11.5	679	2	E85892	hypothetical prote
10	73.5	11.5	1076	1	A35622	hypothetical prote
11	73.5	11.5	7463	2	T36248	nuclear pore prote
12	73	11.4	392	2	F96937	CDA peptidase syntn
13	73	11.4	429	2	T17215	cell wall-associat
14	73	11.4	620	1	W1WLEB	hypothetical prote
15	73	11.4	968	2	T45746	hypothetical prote
16	72.5	11.3	404	1	QOBE13	hypothetical prote
17	72.5	11.3	1075	2	S76433	BMRF1 protein - hu
18	72	11.2	83	2	S10706	cation efflux syst
19	72	11.2	308	2	C83340	urotensin II precu
20	72	11.2	603	2	S22402	hypothetical prote
21	71.5	11.2	243	2	S42533	2-aminobenzate-Co
22	71.5	11.2	393	2	T19977	uroprophyrinogen I
23	71.5	11.2	428	2	R11905	hypothetical prote
24	71.5	11.2	428	2	A81111	probable sulfate a
25	71	11.1	760	1	S07896	sulfate adenylyl tr
26	71	11.1	849	1	H71838	transcription fact
27	71	11.1	1299	2	T00261	MAH2 dehydrogenas
28	70.5	11.0	379	2	T04030	hypothetical prote
29	70.5	11.0	748	2	T49633	glucan 1,4-alpha-g

30	70.5	11.0	1882	2	T00069	hypothetical prote
31	70	10.9	501	2	T48336	hypothetical prote
32	70	10.9	1478	2	S20117	protein kinase BCK
33	69.5	10.8	1478	2	AG0724	sepium site determ
34	69.5	10.8	1553	2	C71257	phenylalanine-tRNA
35	69.5	10.8	946	2	UC7810	inositol 1,4,5-tri
36	69.5	10.8	530	2	G70904	hypothetical prote
37	69	10.8	766	1	A47001	transcription fact
38	69	10.8	772	2	C75579	catalase - Deinoco
39	68.5	10.7	98	2	F83432	regulator in type
40	68.5	10.7	269	2	S36166	paired box transcr
41	68.5	10.7	309	2	AC3508	hypothetical prote
42	68.5	10.7	404	2	A82121	2-oxoglutarate deh
43	68.5	10.7	422	1	A56674	paired box transcr
44	68.5	10.7	436	1	S42234	paired box transcr
45	68.5	10.7	449	2	S07714	T64 protein precur

ALIGNMENTS

RESULT 1
150499
urotensin II-gamma precursor - common carp
C:Species: Cyprinus carpio (common carp)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C:Accession: I50499
R:Ohsako, S.; Ishida, I.; Ichikawa, T.; Deguchi, T.
J. Neurosci. 6, 2730-2735, 1986
A>Title: Cloning and sequence analysis of cDNAs encoding precursors of urotensin II-a
A:Reference number: I50498; MUID:86307061; PMID:2427672
A:Accession: I50499
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-125 <OHS>
A:Cross-references: GB:M14088; NID:9213068; PIDN:AAA49216.1; PID:9213069
C:Superfamily: urotensin II

Query Match 17.9%; Score 115; DB 2; Length 125;
Best Local Similarity 27.9%; Pred. No. 0.00041;
Matches 36; Conservative 22; Mismatches 47; Indels 24; Gaps 4;

QY 7 CCLFLGLNPLLSLPVDTGERTQLPVLEDA-----LRALERTMALQTL 56
DB 9 CSVLTLCSHLAHVPTADWTSGPDSVEAGVNPDDFSVDLNEHLQRAAV---- 63
QY 57 ROTMGTEAGESPEGEAPSTETP--TPRGSMKRAFAQONSNTYLSRLIARTKROKHGAA 114
DB 64 -----AGYSPLESDENIKVPQIPEKALRELLLEKPYRLIPPRLMGSRQFRKRGCG 116
QY 115 PECFWKYCI 123
DB 117 ADCFWKYCI 125

RESULT 2
150498
urotensin II-alpha precursor - common carp
C:Species: Cyprinus carpio (common carp)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
R:Ohsako, S.; Ishida, I.; Ichikawa, T.; Deguchi, T.
J. Neurosci. 6, 2730-2735, 1986
A>Title: Cloning and sequence analysis of cDNAs encoding precursors of urotensin II-a
A:Reference number: I50498; MUID:86307061; PMID:2427672
A:Accession: I50498
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-125 <OHS>
A:Cross-references: GB:M14084; NID:9213066; PIDN:AAA49215.1; PID:9213067
C:Superfamily: urotensin II

Query Match 15.8%; Score 101.5; DB 2; Length 125;

A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A91048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-663 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA836776.1; PID:q13362823; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECS3353

Query Match 11.8%; Score 75.5; DB 2; Length 663;
Best Local Similarity 32.1%; Pred. NO. 19;
Matches 26; Conservative 9; Mismatches 17; Indels 29; Gaps 4;

Qy 33 LPVLEED-ALRAL-----EELERMALLOTROTMGTGEGSPGEGSPSTETPT 79
||| ||| ||| : ||| : ||| ||| |||
Db 588 LPTLNEDSLRSSMAQLHPTTPENDEERQRIYQVLRRTNGIYAG----- 633

Qy 80 PRGSMKRAFAGONSNTVLSRL 100
||| : ||| |||
Db 634 PRGAATR--LGMRRTTLISRM 652

RESULT 8

hypothetical protein b2491 - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: B65025

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
A.: Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: B65025

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-663 <BIAT>

A:Cross-references: GB:AE000335; GB:U00096; NID:q1788821; PIDN:ANCT5544.1; PID:q1788836;
A:Experimental source: strain K-12, substrain MG1655

C:Superfamily: RNA polymerase sigma factor interaction domain homology

F:340-562/Domain: RNA polymerase sigma factor interaction domain homology <SFI>

Query Match 11.8%; Score 75.5; DB 2; Length 663;
Best Local Similarity 32.1%; Pred. NO. 19;
Matches 26; Conservative 9; Mismatches 17; Indels 29; Gaps 4;

Qy 33 LPVLEED-ALRAL-----EELERMALLOTROTMGTGEGSPGEGSPSTETPT 79
||| ||| ||| : ||| : ||| ||| |||
Db 588 LPTLNEDSLRSSMAQLHPTTPENDEERQRIYQVLRRTNGIYAG----- 633

Qy 80 PRGSMKRAFAGONSNTVLSRL 100
||| : ||| |||
Db 634 PRGAATR--LGMRRTTLISRM 652

RESULT 9

hypothetical protein hyfR [imported] - Escherichia coli (strain O157:H7, substrain EDL93

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: E85892

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Illier, L.J.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: E85892

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-679 <STO>

A:Cross-references: GB:AE005174; NID:q1251876; PIDN:AA657601.1; GSPDB:GN00145; UMG:P:237
A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:
A:Gene: hyfR

Query Match 11.5%; Score 73.5; DB 2; Length 679;
Best Local Similarity 32.5%; Pred. NO. 31;
Matches 26; Conservative 8; Mismatches 17; Indels 29; Gaps 4;

Qy 33 LPVLEED-ALRAL-----EELERMALLOTROTMGTGEGSPGEGSPSTETPT 79
||| ||| ||| : ||| : ||| ||| |||
Db 595 LPTLNEDSLRSSMAQLHPTTPENDEERQRIYQVLRRTNGIYAG----- 640

Qy 80 PRGSMKRAFAGONSNTVLSRL 99
||| : ||| |||
Db 641 PRGAATR--LGMRRTTLISRL 658

RESULT 10

nuclear pore protein NUP1 - yeast (Saccharomyces cerevisiae)

N:Alternate names: nucleoporin; protein O3182; protein YOR098c; protein YOR3182c

C:Species: Saccharomyces cerevisiae

C:Date: 22-Jan-1993 #sequence_revision 08-Mar-1996 #text_change 21-Jul-2000

C:Accession: A35622; S61658; S66983

R:Davis, L.I.; Fink, G.R.
Cell 61, 965-978, 1990

A:Title: The NUP1 gene encodes an essential component of the yeast nuclear pore compl

A:Reference number: A35622; MUID:90275616; PMID:2190694

A:Accession: A35622

A:Molecule type: DNA

A:Residues: 1-1076 <NAV>

A:Cross-references: EMBL:M33632; NID:q172055; PIDN:AAA34822.1; PID:q172056

A:Experimental source: strain S288C

R:Benes, V.; Andrade, M.A.; Reichmann, S.; Teodoru, C.; Banreivi, A.; Sander, C.; Valen
submitted to the EMBL data library, December 1995

A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromos

A:Reference number: S61643

A:Accession: S61658

A:Molecule type: DNA

A:Residues: 1-1076 <BN>

A:Cross-references: EMBL:X94335; NID:q1262139; PIDN:CAA64020.1; PID:q1164945

R:Yoss, H.; Benes, V.; Reichmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoorge, W
submitted to the Protein Sequence Database, July 1996

A:Reference number: S66965

A:Accession: S66983

A:Molecule type: DNA

A:Residues: 1-1076 <VOS>

A:Cross-references: EMBL:Z75006; NID:q1420274; PIDN:CAA99295.1; PID:q1420275; GSPDB:G
A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:NUP1; MIPS:YOR098C

A:Cross-references: SGD:S0005624; MIPS:YOR098C

A:Map position: 15R
C:Superfamily: nuclear pore protein NUP1

Query Match 11.5%; Score 73.5; DB 1; Length 1076;
Best Local Similarity 23.7%; Pred. NO. 53;
Matches 28; Conservative 18; Mismatches 49; Indels 23; Gaps 4;

Qy 24 TDGERTLOLPVEEDALRALEELERMALLOTROTMGT-----AGESPGAG- 72
||| ||| ||| : ||| : ||| ||| |||
Db 92 TENTERPPLPIPIORLRLREKQRNRMBELGLIOSTFETPTSSVILGSGKSDGG 151

Qy 73 -----PSTETPRGSMKRAFAGONSNTVLSRLARTKQKHQCAPECFW 119
||| ||| ||| : ||| : ||| ||| |||
Db 152 SYLTSTSPSPKNGSCTROLAKSGEDTNVNGPIILKSLNRSNRK-RFHSQSGTGW 208

RESULT 11

T36248

CDA peptide synthetase I - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 01-Dec-2000

C:Accession: T36248

R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A
 submitted to the EMBL Data Library, March 1999
 A:Reference number: Z21602
 A:Accession: T36248
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-7463 <SAU>
 A:Cross-references: EMBL:AL035640; PIDN:CA838518.1; GSPDB:GN00070; SCOEDB:SC653.03c
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: cdePST; SCOEDB:SC653.03c
 C:Superfamily: acetate-CoA ligase homology; acyl carrier protein homology
 C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
 F:516-1074/Domain: acetate-CoA ligase homology #status atypical <ACLI>
 F:1090-1158/Domain: acyl carrier protein homology <ACP1>
 F:1715-2184/Domain: acetate-CoA ligase homology <ACLI2>
 F:2200-2266/Domain: acyl carrier protein homology <ACP2>
 F:2804-3249/Domain: acetate-CoA ligase homology <ACLI3>
 F:3265-3333/Domain: acyl carrier protein homology <ACP3>
 F:4323-4746/Domain: acetate-CoA ligase homology <ACLI4>
 F:4762-4830/Domain: acyl carrier protein homology <ACP4>
 F:5363-5786/Domain: acetate-CoA ligase homology <ACLI5>
 F:5802-5870/Domain: acyl carrier protein homology <ACP5>
 F:6401-6868/Domain: acetate-CoA ligase homology <ACLI6>
 F:6884-6951/Domain: acyl carrier protein homology <ACP6>
 F:1122,2232,3297,4794,5834,6916/Binding site: phosphopantetheine (Ser) (covalent) #status
 Query Match 11.5% Score 73.5; DB 2; Length 7463;
 Best Local Similarity 25.7%; Pred. No. 4.7e+02;
 Matches 28; Conservative 14; Mismatches 58; Indels 9; Gaps 2;
 Oy 11 FIGLNPILSPVDTGERTQLPYLEEDALRALLELRMALLOTLRQTNGTEAGESPGE 70
 Db 2710 FLRLDLALVADPSRRIQGVNVLGPRERERVLTEWMDTPRRVQGFADHVARHAAERGGH 2769
 Oy 71 AGPSTE-TTPRGRSMKAFAGONSNTVLSRLIARTKQKHOGAARPECF 118
 Db 2770 LAVETAGAAAGGALTYGELNERARLARALLAR-----GAGPERF 2810
 RESULT 12
 cell wall-associated hydrolase [Imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: F96937
 R:Noelling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: F96937
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-392 <KUP>
 A:Cross-references: GB:AE001437; PIDN:AAK78289.1; PID:G15023151; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0308
 Query Match 11.4% Score 73; DB 2; Length 392;
 Best Local Similarity 28.6%; Pred. No. 19;
 Matches 16; Conservative 11; Mismatches 29; Indels 0; Gaps 0;
 Oy 41 LKALELELMALLQTLRQTMGTGAGSPGEGAPSTETPTPRGSMKAFAGONSNTV 96
 Db 230 VRAEKDAEKAQAARLVAAANTPAASAPAKAVAKAQAAPLRGVSHSSFAGSGNDVY 285
 RESULT 13
 T17215
 hypothetical protein DKF2p434H2235.1 - human
 C:Species: Homo sapiens (man)

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T17215
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wlmann, S.
 submitted to the Protein Sequence Database, September 1999
 A:Reference number: Z18723
 A:Accession: T17215
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-429 <POU>
 A:Cross-references: EMBL:AL117404
 A:Experimental source: adult testis; clone DKF2p434H2235
 C:Genetics:
 A:Note: DKF2p434H2235.1
 Query Match 11.4% Score 73; DB 2; Length 429;
 Best Local Similarity 24.5%; Pred. No. 21;
 Matches 27; Conservative 12; Mismatches 41; Indels 30; Gaps 3;
 Oy 28 ERTLOLPVLE-----EDALRALLELE-----RMALLOTLRQTNGTEAGE 66
 Db 260 ERQPDVMDLQELISLSLIKGEDECIEAEKVHYIEKKLRQLRQVSQDLMAAGTQMPA 319
 Oy 67 SP-----GEAGPSTETPTPRGSMKAFAGONSNTVLSRLIARTKQ 107
 Db 320 SPLPSFDEVDSDGDPATSVAPAKKRAVVTTEGEETTESRVPSTRPQ 369
 RESULT 14
 W1MLB2
 E1 protein - bovine papillomavirus type 2
 C:Species: bovine papillomavirus type 2
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 12-Jun-1998
 C:Accession: C31169
 R:Groff, D.E.; Mitra, R.; Lancaster, W.D.
 submitted to GenBank, May 1988
 A:Reference number: A94519
 A:Accession: C31169
 A:Molecule type: DNA
 A:Residues: 1-620 <GRO>
 A:Cross-references: GB:M20219; GB:M19551; NID:g332996
 C:Superfamily: papillomavirus E1 protein
 C:Keywords: early protein; glycoprotein
 F:72,109,173/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 11.4% Score 73; DB 1; Length 620;
 Best Local Similarity 31.5%; Pred. No. 32;
 Matches 23; Conservative 13; Mismatches 27; Indels 10; Gaps 3;
 Oy 35 VLEEDALRALLELRMA---LLOTLRQTMGTGAGSPGEGAPSTETPTPR---GSMKRA 87
 Db 75 VQGNHLEVFQALEKKAGEQLNLKRVKLVGSSENSSGSEA---SETPAKRQKAGAKRRL 131
 Oy 88 FAGONSNTVLSRL 100
 Db 132 FSENEANRVLTPL 144
 RESULT 15
 T45746
 hypothetical protein F24M12.190 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 C:Accession: T45746
 R:Vitale, D.; Liguori, R.; Flores, M.; Argiriotu, A.; De Simone, V.; Mewes, H.W.; Lemc
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23012
 A:Accession: T45746
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-968 <VIT>
 A:Cross-references: EMBL:AL132980
 A:Experimental source: cultivar Columbia; BAC clone F24M12
 C:Genetics:

Tue Mar 11 10:10:38 2003

us-09-831-907a-33.rpr

Page 5

A: Map position: 13
A: Introns: 69/1; 99/1; 132/3; 170/3; 198/1; 220/3; 242/3; 284/2; 396/3; 441/3; 514/1; 81
A: Note: F2M12.190

Query Match	11.4%	Score 73;	DB 2;	Length 966;
Best Local Similarity	27.8%;	Pred. No. 52;		
Matches	27;	Conservative	20;	Mismatches 30;
				Indels 20;
				Gaps 4.

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0Y 14 LNLPLSLPYPTT-----GERTIQPLVEEDALRALEELER*MLLQTLRYOTMGTEAGESP 68
Db 371 LSSPQALVSTTTLALKENKDLQTEKLNKEFVQLQAEKRAVSRIEDLOOI-----GEAP 426
0Y 69 GEAGSTETPTPRGSMKRAFAAGONSNTYLSRLAATR 105
   : : : : :
Db 427 QQELISTDSEQ-----TNNVVLGKGYPKLR 452

```

Search completed: March 10, 2003, 17:47:29
Job time : 15.2973 secs

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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:26:37 ; Search time 6.98108 Seconds
(without alignments)
730.773 Million cell updates/sec

Title: US-09-831-907A-33

Perfect score: 641
Sequence: 1 MDRVPCCLLFTGLNPLSL.....TRKHQKHGAPECFMKYCI 123

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64.1	100.0	123	1	UR2_MOUSE
2	54.1	84.4	123	1	UR2_RAT
3	286.5	44.7	124	1	UR2_HUMAN
4	115	17.9	125	1	UR2G_CYPCA
5	113	17.6	127	1	UR2A_RANRI
6	101.5	15.8	125	1	UR2A_CYPCA
7	81.5	12.7	523	1	E2BD_HUMAN
8	79	12.3	523	1	E2BD_RABIT
9	76	11.9	605	1	HYFR_ECOLI
10	75.5	11.8	670	1	NUPI_YEAST
11	73.5	11.5	1076	1	VEI_BPV2
12	73	11.4	319	1	ACCO_ACTCH
13	72.5	11.3	404	1	EAD_EBV
14	72	11.2	83	1	UR2_PLAFA
15	71.5	11.2	243	1	SUMT_STNP7
16	71	11.1	760	1	OCT1_XENLA
17	70.5	11.0	80	1	P8_RAT
18	70.5	11.0	437	1	PAX6_OREYA
19	70	10.9	1478	1	BCK1_YEAST
20	69.5	10.8	553	1	SYRA_TREPA
21	69.5	10.8	946	1	IP3L_HUMAN
22	69.5	10.8	743	1	OCT1_HUMAN
23	69	10.8	357	1	NDF1_CHICK
24	69	10.7	422	1	PAX6_HUMAN
25	68.5	10.7	422	1	PAX6_MOUSE
26	68.5	10.7	437	1	PAX6_BRARE
27	68.5	10.7	437	1	CLUS_COTJA
28	68.5	10.6	2056	1	CBP1_CAFEL
29	68	10.6	364	1	F812_HUMAN
30	67.5	10.5	524	1	E2BD_MOUSE
31	67	10.5	524	1	E2BD_MOUSE

34	67	10.5	739	1	OCT1_CHICK	P15143	gallus gall
35	66.5	10.4	292	1	CGD3_HUMAN	P30281	homo sapien
36	66.5	10.4	420	1	IE68_HSV11	P04485	herpes simp
37	66	10.3	207	1	FM2_BORPE	P05788	bordecella
38	66	10.3	391	1	P33_RAT	P10361	rattus norv
39	66	10.3	546	1	P2CG_HUMAN	O15355	homo sapien
40	66	10.3	646	1	UVRB_METTH	O25542	methanobact
41	65.5	10.2	416	1	PAX6_COTJA	P47238	coturnix co
42	65.5	10.2	979	1	PTPN_BOVIN	P56722	bos taurus
43	65.5	10.2	1033	1	V328_MYCPN	P75310	mycoplasma
44	65.5	10.2	1093	1	TMF1_HUMAN	P82094	homo sapien
45	65	10.1	339	1	HRDC_STROCO	P18184	streptomyc

ALIGNMENTS

RESULT 1	UR2_MOUSE	STANDARD	PRT	123 AA
AC	Q9QZQ3			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Urotensin II precursor (U-II) (UII).			
GN	UIS2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spinal cord;			
RX	MEDLINE=99416011; PubMed=10486557;			
RA	Colouarn Y., Jegou S., Tostivint H., Vaudry H., Lihmann I.;			
RT	"Cloning, sequence analysis and tissue distribution of the mouse and			
RL	rat urotensin II precursors."			
FEBS Lett.	457:28-32(1999).			
CC	- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).			
CC	- TISSUE SPECIFICITY: BRAIN-SPECIFIC. PREDOMINANTLY EXPRESSED IN			
CC	MOTONEURONS OF THE BRAINSTEM AND SPINAL CORD.			
CC	- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.			
CC	- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL: AF172175; AAD55767.1; -			
DR	MGI: 1346329; Ut52.			
DR	InterPro: IPR001483; Urotensin_II.			
DR	Pfam: PF02083; Urotensin_II; 1.			
DR	PROSITE: PS00964; UROTENSIN_II; 1.			
KW	Hormone; Cleavage on pair of basic residues; Signal.			
FT	SIGNAL	1	20	POTENTIAL.
FT	PROPEP	21	104	POTENTIAL.
FT	PEPTIDE	110	123	UROTENSIN_II.
FT	DISULFID	117	122	BY SIMILARITY.
SO	SEQUENCE	123 AA; 13625 MW; F96486195137F7F4 CRC64;		
Query Match	100.0%; Score 641; DB 1; Length 123;			
Best Local Similarity	100.0%; Pred. No. 5.9e-55;			
Matches 123; Conservative	0; Mismatches 0; Indels			
0; Gaps	0;			
OY	1 MDRVPCCLLFTGLNPLSLPVTDTGERTLOPYLEEDALRLAELEERALLQTRQM 60			
DB	1 MDRVPCCLLFTGLNPLSLPVTDTGERTLOPYLEEDALRLAELEERALLQTRQM 60			
OY	61 GTEAGSPGEGAGSTETPTPRGSMRRFAAGONSNTVLSRLAATRKQKHGAPECFMK 120			

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Db      61  GTEGSGSGAGSTETPTPTPGSMKRAFAAGNSNTVLSRLATRTCRHQHGAAPCEGFWK 120
      |||
QY      121  YCI 123
      |||
Db      121  YCI 123

RESULT 2
UR2_RAT
ID      UR2_RAT      STANDARD;      PRT;      123 AA.
AC      Q9QZQ4;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Urotensin II precursor (U-II) (III).
GN      UTS2.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
PI      [1]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Spinal cord;
RX      MEDLINE=99416011; PubMed=10466557;
RA      Coulouarn Y., Jegou S., Tostivint H., Vaudry H., Lihmann I.;
RT      "Cloning, sequence analysis and tissue distribution of the mouse and
      rat urotensin II precursors."
RL      FEBS Lett. 457:28-32(1999).
CC      -1- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: BRAIN-SPECIFIC.
CC      -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
-----
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-----
DR      EMBL; AF172174; AAD55766.1; -
DR      InterPro; IPR001483; Urotensin_II.
DR      Pfam; PF02083; Urotensin_II; 1.
DR      PROSITE; PS00984; UROTENSIN_II; 1.
KW      Hormone; Cleavage on pair of basic residues; Signal.
FT      SIGNAL          1          20
FT      PROPEP          21          104
FT      PEPTIDE          110          123
FT      DISULFID          117          122
SQ      SEQUENCE      123 AA; 13614 MW; E4F1A8EE124AF1EA CRC64;
      Query Match      84.4%;      Score 541;      DB 1;      Length 123;
      Best Local Similarity      84.6%;      Pred. No. 2.4e+45;
      Matches 104;      Conservative 7;      Mismatches 12;      Indels 0;      Gaps 0.

QY      1  MNRVPCCLLFGLNPLSLPVTPTGERTGLDLPVLEEDALALBELRSMALQTLRTGM 60
      |||
Db      1  MNRVPCCLLFGLNPLSLPVTPTGESSLDLPVLEENALALBELRTALLQTLRTIV 60
      |||
QY      61  GTEAGSGPEAGPSTETPTPTPGSMKRAFAAGNSNTVLSRLATRTCRHQHGAAPCEGFWK 120
      |||
Db      61  GTEAGSGLGQADPSAETPTPTPGSLKRALTGQDSNTVLSRLATRTCRHQHGAAPCEGFWK 120
      |||
QY      121  YCI 123
      |||
Db      121  YCI 123

```

AC 0953399; Q9UKP7.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DR Urotensin II precursor (U-II) (UII).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Spinal cord;
RX MEDLINE=99080095; PubMed=9861051;
RA Coulouarn Y., Lihmann I., Jegou S., Anouar Y., Tostivint H.,
RA Beauvillain J.C., Conlon J.M., Bern H.A., Vaudry H.;
RT "Cloning of the cDNA encoding the urotensin II precursor in frog and
RT human reveals intense expression of the urotensin II gene in
RT motoneurons of the spinal cord";
RL Proc. Natl. Acad. Sci. U.S.A. 95:15803-15808(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99429933; PubMed=10499587;
RA Ames R.S., Sarau H.M., Chambers J.K., Willette R.N., Aiyar N.V.,
RA Romanic A.M., Louden C.S., Foley J.J., Sauermelch C.F., Coatsney R.W.,
RA Ao Z., Disa J., Holmes S.D., Stadel J.M., Martin J.D., Liu W.-S.,
RA Glover G.I., Wilson S., McNulty D.E., Ellis C.E., Elshourbagy N.A.,
RA Shabon U., Trill J.J., Hay D.W.P., Ohlstein E.H., Bergsma D.J.,
RA Douglas S.A.;
RT "Human urotensin-II is a potent vasoconstrictor and agonist for the
RT orphan receptor GPR14".
RL Nature 401:282-286(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Pearce A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: HIGHLY POTENT VASOCONSTRICTOR.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: BRAIN-specific.
CC -I- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.

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DR EMBL: AF104118; AAD13070.1; -
DR EMBL: AF104030; AAD55577.1; -
DR EMBL: Z98884; CAB63148.1; -
DR Genew: HGNC:12636; UTS2.
DR MIM: 604097; -
DR InterPro: IPR001483; Urotensin_II.
DR Pfam: PF02083; Urotensin_II.1.
DR PROSITE: PS00984; UROTENSIN_II.1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 20
FT PROPEP 21 110
FT PEPTIDE 114 124 UROTENSIN II.
FT DISULFD 118 123 BY SIMILARITY.
FT CONFLICT 1 19 MKLSGCLFGLNPL -> METWVHMLCVTSARTH
FT KSTSLCFGHNSYP (IN REF. 2).
FT CONFLICT 24 27 LDSR -> IHDLIL (IN REF. 2).
SQ SEQUENCE 124 AA; 14295 MW; C7A5FC7E9ED0D312 CRC64;

Query Match 44.7%; Score 286.5; DB 1; Length 124;
Best Local Similarity 49.6%; Pred. No. 7.le-21;
Matches 62; Conservative 19; Mismatches 41; Indels 3; Gaps 2.

1 MDKVPCELLFTGLLNPLSLPVTDGTGERLTQLPYLEEDALRALAEELRMALLOTTRQTH 60

I :: ||||| ||||||| : | : | | ||| ||||| ||||| :

Db 1 MYKLASCLLFLGFLNPLSLPLDLSREISPOLSAHPHEDARLPPEELERASLIQILPEML 60
QY 61 CTGAGSPGAGSTPTPTGSRK--APAGONSNTVLRLARTRKQKHGAPECF 118
Db 61 GAERGDILRRADSTNTFNFRGNLRFQDFSGODPNILLSHLLARIMKPKKR-ETPDGF 119
QY 119 WKYCI 123
Db 120 WKYCV 124

RESULT 4
UR2G_CYPCA STANDARD: PRT: 125 AA.
ID UR2G_CYPCA
AC P06580;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE UII gamma precursor [Contains: Urophysin gamma; Urotensin II-gamma].
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_Taxid=7962;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86307061; PubMed=2427672;
RX Ohsako S., Ishida I., Ichikawa T., Deguchi T.;
RT "Cloning and sequence analysis of cDNAs encoding precursors of
RT Urotensin II-alpha and -gamma.";
RL J. Neurosci. 6:2730-2735(1986).
RN [2]
RP SEQUENCE OF 114-125.
RA Muekata E., Ohnaki T., Ichikawa T., McMaster D., Lederis K.;
RL (In) Rich D.H., Gross E. (eds.);
RT Proceedings of the 7th american peptide symposium, pp.69-72,
RL Pierce Chemical Co., Rockford IL (1981).
CC -1- FUNCTION: UROSENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
CC PRECURSOR MAY BE A UROSENSIN BINDING PROTEIN, UROPHYSIN.
CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
CC
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CC
DR EMBL; M14088; AAA49216.1;
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin_II; 1.
DR PROSITE; PS00984; UROSENSIN_II; 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT CHAIN 22 106 UROPHYSIN GAMMA (POTENTIAL).
FT PEPTIDE 114 125 UROSENSIN II-GAMMA.
FT DISULFID 119 124
FT SEQUENCE 125 AA; 13866 MW; E1587DCFC8CB67AD CRC64;

Query Match 17.9%; Score 115; DB 1; Length 125;
Best Local Similarity 27.9%; Pred. No. 0.00022;
Matches 36; Conservative 22; Mismatches 47; Indels 24; Gaps 4;

QY 7 CCLFLGILNPLSLPVDTGERTLOLPVLEEDA-----LRLALEERMLLQTL 56
Db 9 CVALLS-CSHLAHVPTDADMTYSGPDSVEAGCVNPPDFSDNENHLQRAV----- 63
QY 57 ROMMGFAGSPGAGSTPT--TPRGSMRKAFAGONSNTVLRLARTRKQKHGA 114
Db 64 -----AGTSPLESDENIKVPGQIPREALRELEKPYRLIPPRLGMSRRQPRKRGCG 116

QY 115 PECFWKCYI 123
Db 117 ADCFWKCYI 125

RESULT 5
UR2_RANRI STANDARD: PRT: 127 AA.
ID UR2_RANRI
AC P33715; Q9PSX6;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urotensin II precursor (U-II) (U11).
GN UTS2.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8406;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Brain;
RX MEDLINE=99080095; PubMed=9861051;
RA Coulouarn Y., Lihmann I., Jegou S., Anouar Y., Tostivint H.,
RA Beauvillain J.C., Conlon J.M., Bern H.A., Vaudry H.;
RT "Cloning of the cDNA encoding the urotensin II precursor in frog and
RT human reveals intense expression of the urotensin II gene in
RT motoneurons of the spinal cord.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:15803-15808(1998).
RN [2]
RP SEQUENCE OF 115-127.
RA TISSUE=Brain;
RX MEDLINE=93075134; PubMed=1445302;
RA Conlon J.M., O'Harte F., Smith D.D., Tonon M.-C., Vaudry H.;
RT "Isolation and primary structure of urotensin II from the brain of a
RT leopard, the frog Rana ridibunda.";
RL Biochem. Biophys. Res. Commun. 188:578-583(1992).
CC -1- FUNCTION: INVOLVED IN SMOOTH MUSCLE STIMULATING AND ION
CC MOBILIZING ACTIVITIES. IT HAS A SUGGESTED ROLE AS A
CC CORTICOTROPIN-RELEASING FACTOR.
CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM. SPINAL CORD.
CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
CC
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CC
DR EMBL; AF104117; AAD13069.1;
DR PIR; P00445;
DR InterPro; IPR001483; Urotensin_II.
DR Pfam; PF02083; Urotensin_II; 1.
DR PROSITE; PS00984; UROSENSIN_II; 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 16
FT PROPEP 17 111
FT PEPTIDE 115 127
FT DISULFID 121 126 UROSENSIN II.
FT SEQUENCE 127 AA; 14732 MW; FC26B8C90E0C082E CRC64;

Query Match 17.6%; Score 113; DB 1; Length 127;
Best Local Similarity 30.8%; Pred. No. 0.00035;
Matches 40; Conservative 21; Mismatches 59; Indels 10; Gaps 5;

QY 1 MDRVPCCLFLGILNPLSLPVDTGERTLOLPVLEEDA-LRLALEERMLLQTL 58
Db 1 MSKLFPCCLILAGSFCFSRSLPIVPSKSLRLSESLADGDLKSWDETR--LLRLPLM 58
QY 59 TWGTEAGSPGAGSTPT--TPRGSMRKAFAGONSNTVLRLARTRKQKHGA 113

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Db      59 EVDKEA-ERDAEDIFSKEGGLDAYNMDDKELELDKHPRISSLRLQSKDRKFRKRN 117
Oy      114 APCEFWKYCT 123
Db      118 LSECFWKYCV 127

RESULT 6
UR2A_CYPCA STANDARD: PRT: 125 AA.
ID UR2A_CYPCA
AC P04560;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE U11 alpha precursor [contaminates: Urotensin alpha; Urotensin II-alpha].
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=86307061; Pubmed=2427672;
RA Ohsaka S., Ishida I., Ichikawa T., Deguchi T.;
RT "Cloning and sequence analysis of cDNAs encoding precursors of
   urotensin II-alpha and -gamma."
RT J. Neurosci. 6:2730-2735(1986).
RN 12
RP SEQUENCE OF 114-125.
RA Munekata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
RA (in) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th american peptide symposium, pp.69-72,
   Pierce Chemical Co., Rockford IL. (1981).
RL Pierce Chemical Co., Rockford IL. (1981).
CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
   SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
   CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
   PRECURSOR MAY BE A UROTENSIN BINDING PROTEIN, UROPHYSIN.
CC -1- SIMILARITY: BELONGS TO THE UROTENSIN 2 FAMILY.
CC -----
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CC -----
CC EMBL: M14084; AAA49215.1;
DR InterPro: IPR001483; Urotensin-II.
DR Pfam: PF02083; Urotensin-II: 1.
DR PROSITE: PS00984; UROTENSIN-II: 1.
KW Hormone; Cleavage on pair of basic residues; Signal.
FT SIGNAL 1 21
FT CHAIN 22 106 UROPHYSIN ALPHA (POTENTIAL).
FT PEPTIDE 114 125 UROTENSIN II-ALPHA.
FT DISULF 119 124
SQ SEQUENCE 125 AA: 1EP6PF66CA6B35AF CRC64:

Query Match 15.8%; Score 101.5; DB 1; Length 125;
Best Local Similarity 24.3%; Pred. No. 0.0044;
Matches 28; Conservative 23; Mismatches 47; Indels 17; Gaps 2;
Oy 18 LLSLPVDTGERTLQPLVLEED-----ALRALEELERNAALLQTLQTMGTGAGESP 68
Db 19 LVANPVTDTADMTYSGPDSVEAGVSPDDFAVSDLDLORAAVVEYSPLLSRENIKVP 78

Oy 69 GEGGSETEPTPRGSMKRAFAGONSTVLSRLARRKQKHKGAPBEGFWKYCI 123
Db 79 GQ-----IPKEALRELLLEKPYRLIPPSSGLMGSRROFRKRGAGADCFWKYCV 125

RESULT 7
E2BD_HUMAN

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ID E2BD_HUMAN STANDARD: PRT: 523 AA.
AC Q9U110; Q9U95; Q9UBG4; Q9UQ9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Translation initiation factor eIF-2B delta subunit (eIF-2B GDP-GTP
   exchange factor).
GN EIF2B OR EIF2BD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Adrenal gland;
RX MEDLINE=20402571; Pubmed=10931946;
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
   Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
   Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
   Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-H.,
   Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RA "Gene expression profiling in the human hypothalamus-pituitary-adrenal
   axis and full-length cDNA cloning."
RT Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
RN 12
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Wightman P.J., Bonhron D.T.;
RT "cDNA cloning, genomic organization and chromosomal localization of
   the human eIF2B delta subunit."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR
   2-BOUND GDP FOR GTP.
CC -1- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS; ALPHA, BETA, GAMMA,
   DELTA AND Epsilon.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are
   produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE EIF-2B ALPHA/BETA/DELTA SUBUNITS
   FAMILY.
CC -----
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CC -----
CC EMBL: AF112207; AAF17195.1;
DR EMBL: AJ011305; CAB57260.1;
DR EMBL: AJ011306; CAB57261.1;
DR EMBL: AJ011307; CAB57304.1;
DR EMBL: AJ011308; CAB57304.1; JOINED.
DR EMBL: AJ011307; CAB57305.1;
DR EMBL: AJ011308; CAB57305.1; JOINED.
DR Genew; HGNC:3260; EIF2B4.
DR MIM: 606687;
DR InterPro: IPR000649; IF-2B.
DR Pfam: PF01008; IF-2B: 1.
KW Initiation factor; Protein biosynthesis; Alternative splicing.
FT VARSPPLIC 1 10
FT CONFLICT 71 71 FSQA (IN ISOFORM 2).
FT CONFLICT 197 197 MISSING (IN REF. 2).
FT CONFLICT 323 323 S -> T (IN REF. 2).
FT CONFLICT 481 481 L -> S (IN REF. 2).
SQ SEQUENCE 523 AA: F615EAFD816B9E48 CRC64:

Query Match 12.7%; Score 81.5; DB 1; Length 523;
Best Local Similarity 32.1%; Pred. No. 2;
Matches 26; Conservative 10; Mismatches 36; Indels 9; Gaps 2;
Oy 42 RALELEERNAALLQTLQTMGTGAGESPGEAGPSTETPTPRGSMKRAFAGONSTVLSRL 101

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Db 105 RAKEAER-----ALKQARKGEGGPPPKASPTAGETPSGVKRLPEYQVDDLRLRLV 159
 QY 102 ARTKO-----HKQGAPECF 118
 Db 160 KKPERQOVPTRKDYGSKVSLEF 180

RESULT 8

E2BD_RABIT
 ID E2BD_RABIT STANDARD; PRT; 523 AA.
 AC PA111;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Translation Initiation factor eIF-2B delta subunit (eIF-2B GDP-GTP exchange factor).
 GN E1F2B4 OR E1F2BD.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Liver;
 RX MEDLINE=94153999; PubMed=8110836;
 RA Price N.T., Francia G., Hall L., Proud C.G.;
 RT "Guanine nucleotide exchange factor for eukaryotic initiation factor-2. Cloning of cDNA for the delta-subunit of rabbit translation initiation factor-2B."
 RT Biochim. Biophys. Acta 1217:207-210(1994).
 RL -1- FUNCTION: CATALYZES THE EXCHANGE OF EUKARYOTIC INITIATION FACTOR 2-BOUND GDP FOR GTP.
 CC -1- SUBUNIT: COMPLEX OF FIVE DIFFERENT SUBUNITS: ALPHA, BETA, GAMMA, DELTA AND EPSILON.
 CC -1- SIMILARITY: BELONGS TO THE EIF-2B ALPHA/BETA/DELTA SUBUNITS FAMILY.

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 CC -----
 DR EMBL: X75451; CAAS3204.1; ALT_INIT.
 DR InterPro: IPR000649; IF-2B.
 DR Pfam: PF01008; IF-2B; 1.
 KW Initiation factor; Protein biosynthesis
 SQ SEQUENCE 523 AA; 57120 MW; 057895B1E9D25558 CRC64;

Query Match 12.3%; Score 79; DB 1; Length 523;
 Best Local Similarity 31.7%; Pred. No. 3.5;
 Matches 26; Conservative 11; Mismatches 35; Indels 10; Gaps 3;

QY 42 RALEBELEMLLQTLRQMTGEAGSPGEAGPSTETPTTPRSGSMKRAFGQ-NSNTVLSRL 100
 Db 104 RAKEAER-----ALKQARKGEGGPPPKASPTAGETPSGVKRLPEYQVDDLRLRLV 159
 QY 101 LARTRKQ---HKQGAPECF 118
 Db 159 VRKSEROOVPTRKDYGSKVSLEF 180

RESULT 9
 ID VE1_BPV1 STANDARD; PRT; 605 AA.
 AC P03116; O9MMH1;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Replication protein El.
 GN El.

OS Bovine papillomavirus type 1.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10559;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83012974; PubMed=6289124;
 RA Chen E.Y., Howley P.M., Levinson A.D., Seeburg P.H.;
 RT "The primary structure and genetic organization of the bovine papillomavirus type 1 genome."
 RL Nature 299:529-534(1982).
 RN (2)
 RP REQUIREMENT FOR REPLICATION.
 RX MEDLINE=91122053; PubMed=1846806;
 RA Ustav M., Stenlung A.;
 RT "Transient replication of BPV-1 requires two viral polypeptides encoded by the E1 and E2 open reading frames."
 RL EMBO J. 10:449-457(1991).
 RN (3)
 RP CHARACTERIZATION.
 RX MEDLINE=93281701; PubMed=8389467;
 RA Yang L., Mohr I., Fouts E., Lim D.A., Nohaile M., Botchan M.;
 RT "The E1 protein of bovine papilloma virus 1 is an ATP-dependent DNA helicase."
 RL Proc. Natl. Acad. Sci. U.S.A. 90:5086-5090(1993).

CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2 PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
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 CC -----
 DR EMBL: X02346; CAB46511.1; -
 DR PIR: A03663; MIMLEB.
 DR TRANSFAC: T00203; -
 DR InterPro: IPR001177; Papillom_EL.
 DR Pfam: PF00519; E1; 1.
 DR Pfam: PF00524; E1_N; 1.
 KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding; Nuclear protein.
 FT NP_BIND 433 440
 FT SEQUENCE 605 AA; 68190 MW; C840087B8F6060E0B CRC64;

Query Match 11.9%; Score 76; DB 1; Length 605;
 Best Local Similarity 28.9%; Pred. No. 8;
 Matches 24; Conservative 16; Mismatches 33; Indels 10; Gaps 3;

QY 35 VLEBALALELELEMA-----LQTLRQMTGEAGSPGEAGPSTETPTTPR---GSMKRA 87
 Db 59 VFQGNHLEVFPALEKKEAGEOILNLKRVKLSGSSQSSSEA---SETYVKRKSSAKRRL 115
 QY 88 FAGONSNTVLSRLARTKHKQ 110
 Db 116 FAENENANRVLTPLVOYGEGERQ 138

RESULT 10
 ID HYFR_ECOLI STANDARD; PRT; 670 AA.
 AC P71228; P76567; P76976; P76977;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hydrogenase-4 transcriptional activator.
 GN HYFR OR B2491.
 OS Escherichia coli.

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CC Bacteriella:Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562:
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12:
RA Andrews S.C., McClay J., Ambler A., Quail M., Berks B.C., Guest J.R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=9742661; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Siao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsushashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yanagata S., Horiiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT K-12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features."
RL DNA Res. 4:91-113(1997).
CC -1- FUNCTION: REQUIRED FOR INDUCTION OF EXPRESSION OF THE HYDROGENASE-
CC 4 STRUCTURAL GENES.
CC -1- SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR
CC INTERACTION ATP-BINDING DOMAIN.
CC -----
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CC -----
DR EMBL: M63654; AAB88573.1; -.
DR EMBL: AE000335; AAC75544.1; ALP_INIT.
DR EMBL: D90877; BAA16379.1; -.
DR EMBL: D90878; BAA16380.1; -.
DR EcoGene: EG14219; hylR.
DR InterPro: IPR003593; AAA_Atpase.
DR InterPro: IPR003018; GAF.
DR InterPro: IPR002197; HTH_Fls.
DR InterPro: IPR002078; Sig54_interact.
DR Pfam: PF00158; Sigma54_activat; 1.
DR Pfam: PF02954; HTH_8; 1.
DR SMART: SM00382; AAA; 1.
DR SMART: SM00065; GAF; 1.
DR TIGRFAMs: TIGR01199; HTH_Fls; 1.
DR PROSITE: PS00675; SIGMA54_INTERACT_1; 1.
DR PROSITE: PS00676; SIGMA54_INTERACT_2; 1.
DR PROSITE: PS00688; SIGMA54_INTERACT_3; 1.
DR PROSITE: PS50045; SIGMA54_INTERACT_4; 1.
KW Transcription regulation; Activator; DNA-binding; ATP-binding;
KW Complete proteome.
KW DOMAIN 347 576 SIGMA-54 FACTOR INTERACTION (POTENTIAL).
FT NP_BIND 375 382 ATP (POTENTIAL).
FT NP_BIND 438 447 ATP (POTENTIAL).
FT DNA_BIND 641 660 H-T-H MOTIF (BY SIMILARITY).
SQ SEQUENCE 670 AA: 75305 MW: 0EAV38D2DBA96B6 CRC64:
Query Match 11.8%; Score 75.5; DB 1; Length 670;

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QY      24  TDTGERTLQPLVEEDLRALAELEERALLQTLRTQMGTE-----AGESPDEAG- 72
      1: 11 11:11 11 11:11: 11
Best Local Similarity 32.1%; Pred.No.10;
Matches 26; Conservative 9; Mismatches 17; Indels 29; Gaps 4;

Db      595  LPTLNDLSALRSSMAQLHPTTPNDEEERQRIYQVLRETGNCIVAG----- 640
      1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111:
QY      80  PRGSMRKAFPGQNSNTVLSRL 100
      1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111: 1111:
Db      641  PRCAATR-LGMKRTLLSRM 659

RESULT 11
NUPI_YEAST STANDARD: PRT; 1076 AA.
AC P20676;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nucleoporin NUPI (Nuclear pore protein NUPI1).
NUPI OR YOR098C OR YOR182C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RX RA MEDLINE=90275616; PubMed=2190694;
RA Davis L.I., Fink C.R.;
RT "The NUPI gene encodes an essential component of the yeast nuclear
RL pore complex."
RN Cell 61:965-978(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=97344368; PubMed=9200815;
RA Voss H., Benes V., Andrade M.A., Valencia A., Rechmann S., Teodoru C.,
RA Schwager C., Paces V., Sander C., Ansoerge W.;
RL "DNA sequencing and analysis of 130 kb from yeast chromosome XV."
RN Yeast 13:655-672(1997).
CC -I- FUNCTION: ESSENTIAL COMPONENT OF NUCLEAR PORE COMPLEX.
CC NUCLEOPORINS MAY BE INVOLVED IN BOTH BINDING AND TRANSLLOCATION OF
CC THE PROTEINS DURING NUCLEOCYTOPLASMIC TRANSPORT.
CC -I- SUBCELLULAR LOCATION: Nuclear pore complex.
CC -I- DOMAIN: APPEARS TO BE DIVIDED INTO THREE DOMAINS DEFINED BY
CC CENTRALLY LOCATED REPEATING UNITS. FUNCTIONAL N-TERMINAL OF NUPI
CC OR OF NUP2 IS REQUIRED FOR GROWTH.
CC -I- DOMAIN: CONTAINS F-Y-F-G REPEATS.
CC -I- SIMILARITY: TO THE CENTRAL REPEATING UNITS OF NSP1 AND NUP2, AND
CC TO MAMMALIAN P62.
CC
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CC
DR EMBL: M33632; AAA34822.1; -
DR EMBL: X94335; CAA64020.1; -
DR EMBL: 275006; CAA99295.1; -
DR PIR: A35622; A35622.
DR SGD: S0005624; NUPI1.
KM Nuclear Protein; Transport; Repeat.
FT DOMAIN 333 949 29 x 9 AA APPROXIMATE REPEATS.
SQ SEQUENCE 1076 AA; 113581 MW; 4AC23567D2FB53CC CRC64;

Query Match 11.5%; Score 73.5; DB 1; Length 1076;
Best Local Similarity 23.7%; Pred. No. 28;
Matches 28; Conservative 18; Mismatches 49; Indels 23; Gaps 4

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Db 92 TENTERPPLPIQLRLREKQVRNMRRELGIQSTEPSITSSVILGSSKSDSG 151
OY 73 -----PSTETPPRGSMRAFAQONS-----TVLSRLATRKOKHGAPECFW 119
Db 152 SYLCTSSPSPKNSCTROLAGSGEDTNVGLPIKLSKNSNRK-RFHSQSKGTW 208

RESULT 12
ACCO_ACTCH STANDARD; PRT; 319 AA.
ID ACCO_ACTCH STANDARD; PRT; 319 AA.
AC P31237;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate oxidase (EC 1.1.1.1) (ACC oxidase)
DE (Ethylene-forming enzyme) (EFE).
GN ACO.
OS Actinidia chinensis (Klwi) (Yangtiao).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Actinidiaceae; Actinidia.
OX NCBI_TaxID=3625;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Deliciosa;
RX MEDLINE=94105308; PubMed=8278512;
RA MacIarnid C.W., Gardner R.C.;
RT "A cDNA sequence from kiwifruit homologous to 1-aminocyclopropane-1-
RL carboxylic acid oxidase."
CC Plant Physiol. 101:691-692(1993).
CC -1- CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE + O2 =
CC ETHYLENE + HCN + CO(2) + 2 H(2)O.
CC -1- COFACTOR: IRON AND ASCORBATE.
CC -1- PATHWAY: Ethylene biosynthesis; last step.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING FRUIT RIPENING.
CC -1- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC OXIDOREDUCTASES.
CC -----
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CC -----
DR EMBL: M97961; AAA18566.1;
DR InterPro: IPR005123; 2OG-Fer1_Oxy.
DR Pfam: PF03171; 2OG-Fer1_Oxy.
KW Fruit ripening; Ethylene biosynthesis; Oxidoreductase; Iron;
KW Vitamin C; Multigene family.
SQ SEQUENCE 319 AA; 36292 MW; 818FC9551FD98524 CRC64;

Query Match 11.4%; Score 73; DB 1; Length 319;
Best Local Similarity 32.9%; Pred. No. 7.3;
Matches 28; Conservative 13; Mismatches 24; Indels 20; Gaps 5;

OY 18 LLSLPVDTGERTQLPVEDALRAL---EELERNA--LLQTLRQTMGEAGESP--- 68
Db 92 LRLHPVSNISE---IPDLBDHRRKAMKEFAEKLEKLABQLDLLENVGLKGLAKAF 147
OY 69 -GEAGPSTET-----PTPRGSMRK 86
Db 148 YGSKGPTFGTKVSNYPCCPPELIK 172

RESULT 13
ID VEL_BPV2 STANDARD; PRT; 604 AA.
AC P11298;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)

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DE Replication protein E1.
GN E1.
OS Bovine papillomavirus type 2.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10560;
RN [1]
RP SEQUENCE FROM N.A.
RA Groff D.E., Mita R., Lancaster W.D.;
RL Submitted (May-1988) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -----
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CC -----
DR EMBL: M20219; AAA66833.1;
DR PIR: C1169; W1WLB2.
DR InterPro: IPR001177; Papillom_E1.
DR Pfam: PF00519; E1.
DR Pfam: PF00524; E1_N.
KW Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
KW Nuclear protein.
FT NP_BIND 432 439 ATP (POTENTIAL).
SQ SEQUENCE 604 AA; 68077 MW; D2D7036ADE88A9DD CRC64;

Query Match 11.4%; Score 73; DB 1; Length 604;
Best Local Similarity 31.5%; Pred. No. 16;
Matches 23; Conservative 13; Mismatches 27; Indels 10; Gaps 3;

OY 35 VLEEDALRLALELERMA---LLQTLRQTMGEAGESPSTETPTPR---GSMKA 87
Db 59 VFGGHLVEFPALEKAEEDQLNKKRVLVSSGSEA---SETPAKKQAGAKRRL 115
OY 88 FAGONSNTVLSRL 100
Db 116 FSENEANRVLTPL 128

RESULT 14
ID EAD_EBV STANDARD; PRT; 404 AA.
AC P03191;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Early antigen protein D (EA-D).
GN BMRF1..
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tufnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [2]
RP SEQUENCE OF 123-404 FROM N.A.
RX MEDLINE=87284177; PubMed=2441081;
RA Pflizer A.J., Strominger J.L., Speck S.H.;
RT "Characterization of a cDNA clone corresponding to a transcript from

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RT the Epstein-Barr virus BamHI M fragment: evidence for overlapping.
 RT MRNAS: ".
 RL J. Virol. 61:2943-2946(1987).
 RN [3]
 RP IDENTIFICATION OF PROTEIN.
 RX MEDLINE=86062917; PubMed=2999442;
 RA Cho M.-S., Milman G., Hayward S.D.;
 RT "A second Epstein-Barr virus early antigen gene in BamHI fragment M
 RL encodes a 48- to 50-kilodalton nuclear protein.";
 RL J. Virol. 56:860-866(1985).
 CC -1- FUNCTION: TRANS-ACTIVATOR FOR LYTIC CYCLE.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -----
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 CC -----
 CC DR EMBL: V01555; CAA24844.1; .
 CC DR EMBL: M17322; AAA45877.1; .
 DR PIR: A03754; Q08E13.
 DR PIR: S32998; S32998.
 KW Early Protein; Transcription regulation; Activator; DNA-binding;
 KW Nuclear Protein; Antigen.
 SQ SEQUENCE 404 AA; 43373 MW; 533B5D5ECC05F960 CRC64;
 Query Match 11.3%; Score 72.5; DB 1; Length 404;
 Best Local Similarity 24.1%; Pred. No. 11;
 Matches 33; Conservative 14; Mismatches 53; Indels 37; Gaps 4;
 Oy 17 PLTSLPV-----TDMGERTQLPV-----EEDALRALELERMA--- 51
 Db 258 PAVSVPLRFVSGIIVAVAGLLTSAGDLPDLVLFNHASEEAATASTSEPDKSPRV 317
 Oy 52 -----LLOTLRQMTGTEGSPGEAGPSTETPTPGSMKKAFAQONSNTVLSRLA--- 102
 Db 318 QPLGIGLOORPRHTYSPSPRPRTPTWESPAREPSPAPISHSNTALERPLAVQL 377
 Oy 103 ---RTRKQKHQGAPE 116
 Db 378 ARKRTSSSEAROKKHPR 394
 RESULT 15
 UR2_PLAFA STANDARD; PRT: 83 AA.
 ID UR2_PLAFA
 AC P21857;
 DT 01-MAY-1991 (rel. 18, Created)
 DT 01-MAY-1991 (rel. 18, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Urotensin II precursor (U-II) (U-II) (Fragments).
 OS Platicthys flesus (European flounder).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuroneciformes;
 OC Pleuronecoidae; Pleuronectidae; Platicthys.
 OX NCBI_TaxID=8260;
 RN [1]
 RP SEQUENCE.
 RP TISSUE=Urophysals;
 RX MEDLINE=90306357; PubMed=2365069;
 RA Conlon J.M., Arnold-Reed D.E., Baiment R.J.;
 RT "Post-translational processing of prepro-urotensin II.";
 RL FEBS Lett. 266:37-40(1990).
 CC -1- FUNCTION: UROSENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
 CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
 CC CORTICOTROPIN-RELEASING FACTOR. THE NONHORMONAL PORTION OF THIS
 CC PRECURSOR MAY BE A UROSENSIN BINDING PROTEIN, UROPHYSIN.
 CC -1- SIMILARITY: BELONGS TO THE UROSENSIN 2 FAMILY.
 DR PIR: S10706; S10706.

DR InterPro: IPR001483; Urotensin_II.
 DR PROSITE: PS00984; UROSENSIN_II; 1.
 KW Hormone; Cleavage on pair of basic residues.
 FT NON_TER 1 1
 FT PEPTIDE 1 >48 UROPHYSIN (POTENTIAL).
 FT NON_CONS 48 49
 FT NON_CONS 71 72
 FT PEPTIDE 72 83 UROSENSIN II.
 FT DISULFID 77 82
 FT SEQUENCE 83 AA; 9292 MW; 6DD05757BEDF703 CRC64;
 Query Match 11.2%; Score 72; DB 1; Length 83;
 Best Local Similarity 23.7%; Pred. No. 1.8;
 Matches 28; Conservative 11; Mismatches 27; Indels 52; Gaps 5;
 Oy 22 PVTDMGERTQLPV--LEEDALRALELE-----RMALDQLRQMTGTEAGE 66
 Db 2 PTESAEMPRPGPASPALIEGCVGLDLSLSEONYPPOGAGLYATYLEVLEKQ----- 55
 Oy 67 SPGEAGPSTETPTPR-GSMKKAFAQONSNTVLSRLARTRKQKHQGAAPCEFWKTCY 123
 Db 56 -----SLNPFSSVFGIRKQFAG-----TTECFWTKCV 83

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 Job time : 8.98108 secs